





KW cystic fibrosis; diabetes; Parkinson's disease; prostate cancer;  
 KW cardiac disorders; angina; Alzheimer's disease; amnesia; epilepsy;  
 KW schizophrenia; sickle cell anaemia; infertility; hyperglycaemia;  
 KW hypoglycaemia; hypercholesterolaemia; stroke; multiple sclerosis;  
 KW motor neuron disorder; prion disease; metabolic disease;  
 KW developmental disorder; central nervous system; cardiomyopathy;  
 KW hypertension; asthma; AIDS; allergy; anaemia; atherosclerosis;  
 KW atopic dermatitis; diabetes mellitus; osteoarthritis; osteoporosis;  
 KW rheumatoid arthritis; psoriasis; infection; trauma; hepatitis; cancer;  
 KW leukemia; lymphoma.  
 XX OS Homo sapiens.  
 XX PN WO2003016493-A2.  
 XX PD 27-FEB-2003.  
 XX PR 16-AUG-2002; 2002WO-US026323.  
 XX PR 17-AUG-2001; 2001US-0313242P.  
 PR 21-SEP-2001; 2001US-0324782P.  
 PR 02-OCT-2001; 2001US-0328184P.  
 PR 26-OCT-2001; 2001US-0345337P.  
 PR 01-NOV-2001; 2001US-0335638P.  
 PR 13-NOV-2001; 2001US-0332804P.  
 PR 27-NOV-2001; 2001US-033923P.  
 PR 26-APR-2002; 2002US-0375637P.  
 PR 03-MAY-2002; 2002US-0377444P.  
 PR 11-JUN-2002; 2002US-0388180P.  
 XX PA (INCYT-) INCYTE GENOMICS INC.

PI Tang YT, Lal PG, Yue H, Baughn MR, Nguyen DB, Yao MG, Greene BD;  
 PI Borowsky ML, Lee S, Emerling BM, Xu Y, Becha SD, Gorvad AE;  
 PI Azimai Y, Yue H, Elliott VS, Lee EA, Yang J, Lehr-Mason PM;  
 PI Ramkumar J, Lee SY, Faris M, Turner C, Furness M, Buchbinder JL;  
 PI Walia NK, Li JX, Forsythe IJ, Griffin JA, Gietzen KJ, Swarnakar A;  
 PI Hafalia AJA, Lindquist EA, Jackson AA, Wilson AD, Jin P;  
 PI Khare R, Marquis JP;  
 XX WPI; 2003-268319/26.  
 DR N-PSDB; ABX12019.  
 XX PT Novel human transporter and ion channel polypeptides and polynucleotides  
 PT for diagnosing, preventing or treating cell proliferative, transport,  
 PT neurological, muscle and immunological disorders.  
 PS \*Claim 1; Page 216-217; 253pp; English.

XX The invention discloses isolated polypeptides chosen from human  
 CC transporter and ion channel polypeptides, TRICH 1-26, a biologically  
 active or immunogenic fragment and the nucleic acids encoding them. Also  
 CC disclosed are isolated antibodies raised against the TRICH proteins,  
 CC methods for detecting a target polynucleotide in a sample and a  
 CC microarray where at least one element is a TRICH polynucleotide. The  
 CC proteins are useful for screening for agonists or antagonists, which can  
 CC then be used for treating a disease or condition associated with  
 CC decreased or overexpression of functional TRICH in a patient, for  
 CC screening for a compound that modulates the activity of the polypeptide  
 CC or that binds to the polypeptide or as an immunogen for preparing  
 CC antibodies. The polynucleotides are useful for screening for compounds  
 CC which alter expression of a target polynucleotide or for assessing  
 CC toxicity of a test compound. The polypeptides, polynucleotides,  
 CC modulators and antibodies are useful for diagnosis, treatment (e.g. gene  
 CC therapy) and prevention of cell proliferative, transport, neurological,  
 CC muscle and immunological disorders, such as amytrophic lateral  
 CC sclerosis, cystic fibrosis, diabetes, Parkinson's disease, prostate  
 CC cancer, cardiac disorders, angina, Alzheimer's disease, amnesia,  
 CC epilepsy, schizophrenia, sickle cell anaemia, stroke, multiple  
 CC hyperglycaemia, hypoglycaemia, hypercholesterolaemia, metabolic disease of the  
 CC scleroses, motor neuron disorder, prion disease, nervous system, development disorders of the central nervous system,  
 CC cardiomyopathy, hypertension, asthma, AIDS, allergies, anaemia,

CC atherosclerosis, atopic dermatitis, diabetes mellitus, osteoarthritis, CC osteoporosis, rheumatoid arthritis, psoriasis, infections, trauma, CC hepatitis and cancers, including leukemia and lymphoma. The sequences CC presented in ABG75819-ABG75844 are the TRICH proteins of the invention XX	Sequence 507 AA:
	Query Match 99.9%; Score 2466; DB 6; Length 507; Best Local Similarity 99.8%; Pred. No. 1.7e-257; Matches 475; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSTQRLENDYDSSSTDVSDBESPEGLANLSSPSSYQRGQSNTTWQTLHLIKGK 60	Db 32 LSTQRLENDYDSSSTDVSDBESPEGLANLSSPSSYQRGQSNTTWQTLHLIKGK 91
Qy 61 IGTGLIGLPLAVRNAGTVMGPISLITLIGVAVHCMGTLVCKAHFCCRNLNSFVTDGDTV 120	Db 92 IGTGLIGLPLAVRNAGTVMGPISLITLIGVAVHCMGTLVCKAHFCCRNLNSFVTDGDTV 151
Qy 121 MYGLLESSPCMSLRLNRAHMGRRVVDFFLIVTOLGFCCVYFVFLADNFQVTEAANGTNNC 180	Db 152 MYGLLESSPCMSLRLNRAHMGRRVVDFFLIVTOLGFCCVYFVFLADNFQVTEAANGTNNC 211
Qy 181 HNNETVILTPIMDSRLYMLSLPFLVLLVFLRNRLAISLTSLLANTMVLSLVMIYOFIV 240	Db 212 HNNETVILTPIMDSRLYMLSLPFLVLLVFLRNRLAISLTSLLANTMVLSLVMIYOFIV 271
Qy 241 QRIDPSHLPLAVPAWKTYPFLFGTALFSSFEGLGMVPLENKMDPKRFLPLYLGMVIVT 300	Db 272 QRIDPSHLPLAVPAWKTYPFLFGTALFSSFEGLGMVPLENKMDPKRFLPLYLGMVIVT 331
Qy 301 ILYISIGCLGILQGANIQLGQGANIQLQSYKLLYQSYKLLYQSYKLLYQSYKLLYQSYKLLYQPAELIIP 360	Db 332 ILYISIGCLGILQGANIQLGQGANIQLQSYKLLYQSYKLLYQSYKLLYQSYKLLYQSYKLLYQSYKLLYQPAELIIP 391
Qy 361 FFVSRAPERHCBLVLDLLEVTRVTCILIPRLDVLVSGSYSSALALIIPPLLE 420	Db 392 FFVSRAPERHCBLVLDLLEVTRVTCILIPRLDVLVSGSYSSALALIIPPLLE 451
Qy 421 VTTFFSEGMSPLTIFKDALISLGFGVWVGTYEALYELQPSNAPFINSTCAFI 476	Db 452 VTTFFSEGMSPLTIFKDALISLGFGVWVGTYEALYELQPSNAPFINSTCAFI 507

## RESULT 4

ABP96441  
 ID ABP96441 standard; protein; 476 AA.

XX ABP96441;

AC ABP96441;

DT 02-JUN-2003 (first entry)

XX Human trandorin 3 protein SEQ ID NO:21.

DE DE

KW Neuroprotective; nootropic; cerebroprotective; analgesic; gene therapy;

KW central nervous system disorder; CNS disorder; multiple sclerosis;  
 KW nerve injury; neuropathic pain; stroke; trauma; non-CNS disorder; trand;

KW trandorin; human; tramadol 3; chromosome 5.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FH Misc-difference 356  
 FT /note= "encoded by GAG"

XX WO2003016502-A2.

XX PD 27-FEB-2003.

XX PT 21-AUG-2002; 2002WO-US026637.

XX PR 21-AUG-2001; 2001US-0313907P.

XX PR 21-AUG-2002; 2002US-00225010.



CC assays, detection assays, predictive medicine, and in methods of treatment. NOVX is useful as immunogen, to screen for potential antagonists compounds, and as bait protein in a two-hybrid or three-hybrid assay. NOVX NA' is useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. The cell is useful for producing non-human transgenic animals. Ab is useful for isolating, and purifying NOVX and to monitor protein levels in tissue as part of a clinical testing procedure. The present sequence represents a NOVX protein

XX Sequence 496 AA;

Query Match 99.6%; Score 2460; DB 6; Length 496;  
Best Local Similarity 99.8%; Pred: No. 7.4e-257;  
Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 M5TQRLRNEDYHDYSSTDVSPESPESEGCLANNLSSPSSYXQRFQGSNSTTWFQTLIHLKGK 60

Db 21 M5TQRLRNEDYHDYSSTDVSPESPESEGCLANNLSSPSSYXQRFQGSNSTTWFQTLIHLKGK 80

Qy 61 IGTGLIGLPLAVLKNGIIVMPGPISSLIIIGIAVHCMGILVKCAHHFCRRLNKSFDYGDIV 120

Db 81 IGTGLIGLPLAVKNAIGIVMPGPISSLIIIGIAVHCMGILVKCAHHFCRRLNKSFDYGDIV 140

Qy 121 MYGLBSSPSCSWSLRLRNHAHMGREVVDFPLVITOLGFCCVYFVLADNFQKQVIEAANGTTNNC 180

Db 141 MYGLBSSPSCSWSLRLRNHAHMGREVVDFPLVITOLGFCCVYFVLADNFQKQVIEAANGTTNNC 200

Qy 181 HNNETVILTPMDRLYMLSLPFLVLYVFTIRNLRLSISFSLLANITMVLISLVMYQFIV 240

Db 201 HNNETVILTPMDRLYMLSLPFLVLYVFTIRNLRLSISFSLLANITMVLISLVMYQFIV 260

Qy 241 QRIDPSHLPVAPWKTYPFLFGTAIFSFEGIGNVILPLENKMDPRKFPLILYLGAVIVT 300

Db 261 QRIDPSHLPVAPWKTYPFLFGTAIFSFEGIGNVILPLENKMDPRKFPLILYLGAVIVT 320

Qy 301 ILYISIIGCLGCLGQFGANIQGSIITLNLPCNQLYQSVKLLYSIGIFFTYAALQFYVPAEIIIP 360

Db 321 ILYISIIGCLGCLGQFGANIQGSIITLNLPCNQLYQSVKLLYSIGIFFTYAALQFYVPAEIIIP 380

Qy 361 FFVSRAPHECLVVDLFLVFTVTLVCLTCLAILIPRLDVLISLVGSSYSSSALALIIPPLE 420

Db 381 FFVSRAPHECLVVDLFLVFTVTLVCLTCLAILIPRLDVLISLVGSSYSSSALALIIPPLE 440

Qy 421 VTTFYSSEGMSPLITFKDALISLILGFVFGVGYTEAUYELIOPSNAPIFINSTCAFI 476

Db 441 VTTFYSSEGMSPLITFKDALISLILGFVFGVGYTEAUYELIOPSNAPIFINSTCAFI 496

Qy 6 AA014191 standard; protein; 568 AA.

XX AA014191;

XX 03-MAY-2002 (first entry)

XX Human transporter and ion channel TRICH-8.  
XX Human; transporter and ion channel; TRICH; transport disorder;  
KW neurological disorder; muscle disorder; immunological disorder;  
KW cell proliferative disorder; neuroprotective; nootropic;  
KW cerebroprotective; immuno suppressive; cytostatic; respiratory; muscular;  
KW gene therapy.  
XX Homo sapiens.  
XX WO200204520-A2.  
XX 17-JAN-2002.  
PF 05-JUL-2001; 2001WO-US021448.

PR 07-JUL-2000; 2000US-0216547P.  
PR 14-JUL-2000; 2000US-021232P.  
PR 21-JUL-2000; 2000US-022112P.  
PR 28-JUL-2000; 2000US-0221839P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX PI Raumann BE, Thornton M, Ding L, Yue H, Tang YT, Harland L;  
PI Burford N, Greene BD, Sanjanwala MS, Bauchin MR, Yao MG, Yang J;  
PI Patterson C, Gandhi AR, Hatalia AJA, Triboulet CM, Walia NK;  
PI Au-Young J, Walsh RT, Ramkumar J, Lu Y, Lu DM, Azimzai Y, Lal P;  
PI Elliott VS, Nguyen DB, Xu Y, Seilhamer JJ, Borowsky ML, Khan FA;  
PI Kearney L, Thangavelu K, Das D, Policky JL;  
XX WPI; 2002-205369/26.  
DR N-PSDB; AAL44574.  
XX  
CC The present invention provides the protein and coding sequences of a number of human transporter and ion channel proteins, designated TRICH-1-TRICH-32. The sequences can be used in the treatment of transport, neurological, muscle, immunological and cell proliferative disorders. The present sequence is a protein of the invention  
CC  
XX  
PS Claim 1; Page 155-156; 230pp; English.  
XX  
CC The present invention provides the protein and coding sequences of a number of human transporter and ion channel proteins, designated TRICH-1-TRICH-32. The sequences can be used in the treatment of transport, neurological, muscle, immunological and cell proliferative disorders. The present sequence is a protein of the invention  
CC  
XX  
SQ Sequence 568 AA;  
Query Match 97.3%; Score 2402.5; DB 5; Length 568;  
Best Local Similarity 88.3%; Pred. No. 1.5e-250;  
Matches 474; Mismatches 0; Indels 2; Gaps 2;  
Db 32 MSTQRRLRNEDYHDYSSTDVSPESSEGCLANNLSSPSSYQRFQGSNSTTWFQTLIHLKGK 91  
Qy 1 MSTQRRLRNEDYHDYSSTDVSPESSEGCLANNLSSPSSYQRFQGSNSTTWFQTLIHLKGK 60  
Db 92 IGTGLIGLPLAVKNGIIVMPGPISSLIIIGIAVHCMGILVKCAHHFCRRLNKSFDYGDIV 120  
Qy 32 MSTQRRLRNEDYHDYSSTDVSPESSEGCLANNLSSPSSYQRFQGSNSTTWFQTLIHLKGK 91  
Qy 61 IGTGLIGLPLAVKNGIIVMPGPISSLIIIGIAVHCMGILVKCAHHFCRRLNKSFDYGDIV 120  
Db 121 MYGLBSSPSCSWSLRLRNHAHMGREVVDFPLVITOLGFCCVYFVLADNFQKQVIEAANGTTNNC 180  
Db 152 MYGLBSSPSCSWSLRLRNHAHMGREVVDFPLVITOLGFCCVYFVLADNFQKQVIEAANGTTNNC 211  
Qy 181 HNNETVILTPMDRLYMLSLPFLVLYVFTIRNLRLSISFSLLANITMVLISLVMYQFIV 240  
Db 212 HNNETVILTPMDRLYMLSLPFLVLYVFTIRNLRLSISFSLLANITMVLISLVMYQFIV 271  
Qy 241 QRIDPSHLPVAPWKTYPFLFGTAIFSFEGIGNVILPLENKMDPRKFPLILYLGAVIVT 300  
Db 272 QRIDPSHLPVAPWKTYPFLFGTAIFSFEGIGNVILPLENKMDPRKFPLILYLGAVIVT 331  
Qy 301 ILYISIIGCLGCLGQFGANIQGSIITLNLPCNQLYQSVKLLYSIGIFFTYAALQFYVPAEIIIP 360  
Db 332 ILYISIIGCLGCLGQFGANIQGSIITLNLPCNQLYQSVKLLYSIGIFFTYAALQFYVPAEIIIP 391  
Qy 361 FFVSRAPHECLVVDLFLVFTVTLVCLTCLAILIPRLDVLISLVGSSYSSSALALIIPPLE 420  
Db 392 FFVSRAPHECLVVDLFLVFTVTLVCLTCLAILIPRLDVLISLVGSSYSSSFLA 451  
Qy 387 -----C-----IILALIPRLDVLISLVGSSYSSSALALIIPPLE 419  
Db 452 HPWLSPRCESSWVSCRDTVVWFGRLNLIPRLDVLISLVGSSYSSSALALIIPPLE 511  
Qy 420 EYTTFYSSEGMSPLTIFKDALISLILGFVFGVGYTEADGTSGSAPLVFVSSSFLA 476  
Db 512 EYTTFYSSEGMSPLTIFKDALISLILGFVFGVGYTEAUYELIOPSNAPIFINSTCAFI 568

ABU52587	standard; protein; 500 AA.	CC disorder in a subject, preferably human. Ab is useful for determining the presence or amount of NOVX in a sample. NOVX is useful for identifying an agent that binds to NOVX. NOVX NA or ab is useful for treating metabolic disorders, diabetes, cardiomyopathy, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's disease, immune disorders, haematopoietic disorders, and various dyslipidemias, metabolic disturbances associated with obesity, the metabolic syndrome X and wasting disorders associated with chronic diseases, various cancers, endocrine, connective tissue, blood, vascular, skin, renal, bone, brain, muscle disorders, or bacterial, fungal, protozoal or viral infections. NOVX, NOVX NA or ab is useful in screening assays, detection assays, predictive medicine, and in methods of treatment. NOVX is useful as an immunogen, to screen for potential antagonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. NOVX NA is useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. The cell is useful for isolating, and purifying NOVX and to monitor protein levels in tissue as part of a clinical testing procedure. The present sequence represents a NOVX protein.
AC ABU52587;		CC
XX	04 - MAR - 2003 (first entry)	CC
CC	Human NOVX protein, NOV7a.	CC
KW	Human; immunogen; NOVX; metabolic disorder; diabetes; cardiomyopathy; obesity; infectious disease; anorexia; neurodegenerative disorder;	CC
KW	Alzheimer's disease; Parkinson's disease; immune disorder;	CC
KW	haematopoietic disorder; dyslipidaemia; metabolic disturbance; metabolic syndrome X; wasting disorder; cancer; gene therapy; SNP; single nucleotide polymorphism.	CC
XX	Homo sapiens.	CC
OS		CC
PH	Key difference 173	CC
FT	/note= "May be val as a result of a single nucleotide polymorphism"	CC
FT		XX
XX	WO200281518-A2.	Sequence 500 AA;
XX	*17-OCT-2002.	Query Match 97.1%; Score 2398; DB 6; Length 500;
PD		Best Local Similarity 97.5%; Pred. No. 3.3e-250; Mismatches 0; Indels 12; Gaps 3;
XX	21 - FEB - 2002; 2002WO-US0053374.	Matches 472; Conservative 0; Mismatches 0;
XX	21 - FEB - 2001; 2001US - 02 - 70220P.	Qy 1 M5T0LRNEDYHDYSSTDVSPEESPSEGANNLSSPGSYQRFGSNNTTWFQTLIHLILKCN 60
PR	21 - FEB - 2001; 2001US - 02 - 70523P.	Db 21 M5T0LRNEDYHDYSSTDVSPEESPSEGANNLSSPGSYQRFGSNNTTWFQTLIHLILKGN 80
PR	23 - FEB - 2001; 2001US - 02 - 70797P.	Qy 61 IGRGLGLPLAVRNAGIYNGPISLIIIGIVAHCMGLIYKCAHHFCCRLINKSFYDGDYI 120
PR	23 - FEB - 2001; 2001US - 02 - 70810P.	Db 81 IGRGLGLPLAVRNAGIYNGPISLIIIGIVAHCMGLIYKCAHHFCCRLINKSFYDGDYI 140
PR	08 - MAR - 2001; 2001US - 02 - 74295P.	Qy 121 MYGLESSPCSWLRLNHAHKGRRVVDPLFLIVTOLGFCVYFVFLADNFKQVIEAANGTTNC 180
PR	16 - MAR - 2001; 2001US - 02 - 76400P.	Db 141 MYGLESSPCSWLRLNHAHKGRRVVDPLFLIVTOLGFCVYFVFLADNFKQVIEAANGTTNC 200
PR	26 - MAR - 2001; 2001US - 02 - 76777P.	Qy 181 HNNETVILTPMDSRILYMLSFLPFLVLFIRNLRLSISFLSANITMLVSLMIVYQFLV 240
PR	04 - APR - 2001; 2001US - 0281521P.	Db 201 HNNETVILTPMDSRILYMLSFLPFLVLFIRNLRLSISFLSANITMLVSLMIVYQFLV 260
PR	25 - APR - 2001; 2001US - 0286548P.	Qy 241 -----ORIDPDSHLPLIVAPKTKYPLFFGTAIFSFEGIMVLPENKMKDPRKFPLIL 292
PR	17 - MAY - 2001; 2001US - 0291765P.	Db 261 FRYMLSVFQRIDPDSHLPLIVAPKTKYPLFFGTAIFSFEGIMVLPENKMKDPRKFPLIL 320
PR	10 - AUG - 2001; 2001US - 0311595P.	Qy 293 YLGIVVITVLYISLGCLGYLQFGANIQCSITNLPNCLYQSYKLLYSGIFFTYALQY 352
PR	13 - AUG - 2001; 2001US - 0311980P.	Db 321 YLGIVVITVLYISLGCLGYLQFGANIQCSITNLPL--LYQSYKLLYSGIFFTYALQY 377
PR	10 - SEP - 2001; 2001US - 0318526P.	Qy 353 VPAEIIIPPFVSRAPHECBLVVDLFVRLVCLTCILAILPDLVLVSGVSYSSALA 412
PR	17 - SEP - 2001; 2001US - 0322712P.	Db 378 VPAEIIIPPFVSRAPHECBLVVDLFVRLVCLT-ILAILPDLVLVSGVSYSSALA 436
PR	18 - OCT - 2001; 2001US - 03310307P.	Qy 413 LIIPPLLEVTTTFSEGMSPLTIPKDALISLGFGVYGTBYALYELIOPSNAPIFINST 472
PA	(CUBA-) CURAGEN CORP.	Db 437 LIIPPLLEVTTTFSEGMSPLTIPKDALISLGFGVYGTBYALYELIOPSNAPIFINST 496
PI	Pena CEA, Shimkets RA, Li L, Shenoy SG, Kekuda R, Spytek KA; Vernet CM, Malynanker UL, Guo X, Gusev VY, Casman SJ, Boldog PL; Furrak K, Tchernev VT, Patturajan M, Gangolli EA, Padigaru M, Liu X; Baumgartner JC, Gerlach VL, Spaderna SK, Zethusen BD; WPI, 2003-046859/04.	Qy 473 CAFI 476
XX	New isolated NOVX polypeptide useful for treating cardiomyopathy, atherosclerosis, metabolic disorders, diabetes, obesity, infectious disease, anorexia, neurodegenerative disorders, Alzheimer's disease and cancer.	Db 497 CAFI 500
PS	Claim 1; Page 56; 479pp; English.	DE Human vG51.
XX	The invention relates to an isolated polypeptide termed NOVX (NOV1, 2a, CC 2b, 3a, 3b, 4a, 4b, 5, 6, 7a-c, 8a-e, 9a-b, 10, 11, 12a-c, 13, 14, 15, 16-a-d, 17a-b, 18, 19, 20a-b, 21-30) appearing as ABU52624, a variant of NOVX, a mature form of NOVX, and a variant of the mature form of NOVX. Also included are a nucleic acid molecule (NOVX NA) encoding NOVX, or a fragment or complement of NOVX NA, a vector comprising NOVX NA, a cell comprising the vector, an anti-NOVX antibody (ab), determining the presence or amount of NOVX or NOVX NA in a sample, and identifying an agent that binds or modulates the expression or activity of NOVX. NOVX, NOVX NA or ab is useful for treating or preventing a NOVX-associated	RESULT 8 ABB76941 ID ABB76941 standard; protein: 476 AA. AC ABB76941; DT 22 - JUL - 2002 (first entry) XX

XX	Antiasthmotic; anxiolytic; antiepileptic; antihypertensive; human;	Qy	421 VTTFVSEGMSPLTIFKDALISILGTVGVFTYEALEYLIQPSNAPIFINSTCAPI	476
KW	psychotropic; glutamate transporter; transporter: GABA;	Db	421 VTTFVSEGMSPLTIFKDALISILGTVGVFTYEALEYLIQPSNAPIFINSTCAPI	476
KW	gamma-aminobutyric acid transporter; GABA transporter; neurotransmitter;			
KW	asthma; anxiety; epilepsy; hypertension; psychiatric disorder;			
KW	neurotic disorder; VG51.			
XX	Homo sapiens.			
XX	WO200071709-A1.	RESULT 9		
XX	DR	ADF90169	421 VTTFVSEGMSPLTIFKDALISILGTVGVFTYEALEYLIQPSNAPIFINSTCAPI	476
XX	PN	ID	standard; protein; 476 AA.	
XX	XX	XX		
XX	PD	AC	ADF90169;	
XX	30-NOV-2000.	XX		
XX	PF	DT	26-FEB-2004 (first entry)	
XX	19-MAY-2000; 2000WO-FR001383.	XX		
XX	PA (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.	DE	Human transporter homologue seq id 7.	
XX	PR 21-MAY-1999; 99FR-00006525.	XX		
XX	PA	KW	peptide therapy; transporter; human.	
XX	PI	XX		
XX	GIROS B, Gasnier B, Sagne C, El Mestikawy S, Hamon M;	OS		
XX	WPI: 2001-025160/03.	XX		
XX	DR	PN		
XX	N-PSDB; ABL57930.	11-SEP-2003.		
XX	PS	XX		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
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XX	PS	BEASLEY E M.		
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XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
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XX	PS	(WEIM/)		
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XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
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XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
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XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		
XX	PS	PA		
XX	PS	(BEAS/)		
XX	PS	BEASLEY E M.		
XX	PS	PA		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(WEIM/)		
XX	PS	WEI M.		
XX	PS	PA		
XX	PS	(YANG/)		
XX	PS	YAN C.		
XX	PS	PA		
XX	PS	(MERR/)		
XX	PS	MERKLOV G V.		
XX	PS	PA		
XX	PS	(KETC/)		
XX	PS	KETCHUM K A.		
XX	PS	PA		
XX	PS	(DFRA/)		
XX	PS	DI FRANCESCO V.		

Db	181 HNNETVILDPPTMDSRSLYMSFLPPEVLLFIRNLRLALSFSLLANITMLVSLWMIYQFIV 240	Qy	1 MSTORLRNEDYHDYSSTDVSPEESPSEGNNLNSPQGSYORGOSNSTTWFOTLHLRKCN 60
Qy	241 QRIDPPSHLPLVAPWKTYPLFFGTAIFSEPGIGMVLPLENKMDPRKEPLILYGMIVT 300	Db	1 MSTQRLRNEDYHDYSSTDVSPEESPSEGNNLNSPQGSYORGOSNSTTWFOTLHLRKCN 60
db	241 QRIDPPSHLPLVAPWKTYPLFFGTAIFSEPGIGMVLPLENKMDPRKEPLILYGMIVT 300	Qy	61 IGTGLGLPLAKVNGAIVMGPISLILIGIVATHCMGLVKAHHFCRRLNKSEFVDYGPDTV 120
Qy	301 ILYSLGCGCYLQGANIGSITINLNPWMLQSYKLLYSIGIIFTYALQFYVPAEILIP 360	Db	61 IGTGLGLPLAKVNGAIVMGPISLILIGIVATHCMGLVKAHHFCRRLNKSEFVDYGPDTV 120
Db	301 ILYSLGCGCYLQGANIGSITINLNPWMLQSYKLLYSIGIIFTYALQFYVPAEILIP 360	Qy	121 MYCLESSEPSWLNRHAWGRVUDFLFLITQFLGFCVYFVLADNFQVIEANGTTNC 180
Qy	361 FFVSRAPAECELYVDFLFLTRVLCILCTAILIPRDVLTISLGVSSSALALIPPLE 420	Db	121 MYCLESSEPSWLNRHAWGRVUDFLFLITQFLGFCVYFVLADNFQVIEANGTTNC 180
Db	361 VIVSWVCKCTMLDGISSAMLKTCCTAILIPRDVLTISLGVSSSALALIPPLE 420	Qy	181 HNNETVILTPMDSRSLYMSFLPFLVLFIRNLRLALSFSLLANITMLVSLWMIYQFIV 240
Qy	421 VTTFSEGMSPPLITIFKDALIISLISLGFGFVGTVYEALYELIQPSNAPINSTCAFI 476	Db	181 HNNETVILTPMDSRSLYMSFLPFLVLFIRNLRLALSFSLLANITMLVSLWMIYQFIV 240
Db	421 VTTFSEGMSPPLITIFKDALIISLISLGFGFVGTVYEALYELIQPSNAPINSTCAFI 476	Qy	241 QRIDPSHLPYAPWKTYPLFFGTAIFSEPGIGMVLPLENKMDPRKEPLILYGMIVT 300
RESULT 10			
ADR03804	ADR03804 standard; protein; 476 AA.	Qy	301 ILYISLGCGYLOFGANIQGSITINLNPWMLQSYKLLYSIGIIFTYALQFYVPAEILIP 360
ID	ADR03804	Db	301 ILYISLGCGYLOFGANIQGSITINLNPWMLQSYKLLYSIGIIFTYALQFYVPAEILIP 360
XX		Qy	361 FFVSRAPAECELYVDFLFLTRVLCILCTAILIPRDVLTISLGVSSSALALIPPLE 420
AC	ADR03804;	Db	361 VTTFSEGMSPPLITIFKDALIISLISLGFGFVGTVYEALYELIQPSNAPINSTCAFI 476
XX	21-OCT-2004 (first entry)	Qy	421 VTTFSEGMSPPLITIFKDALIISLISLGFGFVGTVYEALYELIQPSNAPINSTCAFI 476
XX	Human homologue of novel transporter protein.	Db	421 VTTFSEGMSPPLITIFKDALIISLISLGFGFVGTVYEALYELIQPSNAPINSTCAFI 476
XX	Human; transporter.		
XX	Homo sapiens.	RESULT 11	
OS	US2004146887-A1.	ADA55508	ADA55508
PN		ID	ADA55508 standard; protein; 434 AA.
XX		XX	
PD	29-JUL-2004.	AC	ADA55508;
XX		XX	
PF	07-OCT-2003; 2003US-00679362.	DT	20-NOV-2003 (first entry)
XX		XX	
PR	22-DEC-2000; 2000US-0257175P.	DB	Human protein, SEQ ID 3076.
PR	14-MAR-2001; 2001US-00805456.	XX	
XX		XX	
(APPL-)	APPLERA CORP.	KW	Cytostatic; Anti-inflammatory; Osteoprotective; Nootropic;
XX		KW	KW Gene therapy; human; secretory protein; membrane proteins; cancer; inflammatory disease; osteoporosis; neurological disease.
Wei, M.	Yan, C.	XX	XX Homo sapiens.
Merklov, G.	Ketchum, KA.	OS	XX PN EPI1293569-A2.
Difrancesco, V.	Beasley, EM;	XX	XX PD 19-MAR-2003.
XX		XX	XX PP 21-MAR-2002; 2002EP-00006586.
WPI:	2004-552659/53.	XX	XX PR 14-SEP-2001; 2001JP-00328381.
XX	New nucleic acid encoding human transporter peptides, useful for preparing agents for treating a disease or condition mediated by human transporters.	XX	XX PR 24-JAN-2002; 2002US-0350435F.
PT		XX	XX PA (HELI-) HELIX RES INST.
PT		XX	XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX	Disclosure; SEQ ID NO 7; 62pp; English.	PI	Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S;
CC	The invention relates to a new isolated nucleic acid comprising a sequence encoding a transporter protein (appearing as ADR3799) and appearing as ADR03798 (the cDNA) or ADR03800 (the gene). Also included are a vector comprising the isolated nucleic acid, a host cell containing the vector, producing the polypeptide, detecting the presence of the nucleic acid in a sample and an isolated human peptide having a sequence that shares at least 70% homology with ADR3799. The gene encoding the human transporter is located on chromosome 5. The peptide is useful for preparing agents for treating a disease or condition mediated by a human transporter protein. The present sequence represents a homologue of the transporter protein.	PI	Yamamoto, J., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I;
CC	XX	PI	XX PI Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K., Masuho, Y;
CC	XX	DR	XX DR WPI; 2003-395539/38.
XX	Sequence 476 AA;	XX	XX N-BSDB; ADA51869.
SQ	Query Match 94.1%; Score 2324; DB 8; Length 476; Best Local Similarity 94.5%; Pred. No. 3.8e-242; Mismatches 9; Matches 450; Conservative 17; Indels 0; Gaps 0;	PT	New polynucleotides encoding full-length polypeptides, e.g., secretary and/or membrane proteins, useful for developing medicines for diseases in which the gene is involved, or as target molecules for gene therapy.
PS	Claim 14; SEQ ID NO 3076; 205pp; English.	PT	XX



XX	Sequence 475 AA;	Query	Match	86.9%	Score	2146.5;	DB	6;	Length	475;
5Q			Best Local Similarity	85.7%	Pre 6..3e-223;					
	Matches 408; Conservatve	36;	Mismatches	31;	Indels	1;	Gaps	1		
Qy		1	MSTORLRNEDYHDYSSTDVSPSEGPINLSSPGSYQRGOSNSTTWFOQLHLKGNN	60						
Ddb		1	MSTORLRNEDYHDYSSTDVSPSEGPINLSSPGSYQRGOSNSTTWFOQLHLKGNN	59						
Qy		61	IGCGLLGLPLAVKAGIYMGPIISLLIGVAVHMGILLYKCAAHFCRPLINKSFYDGDY	120						
Ddb		60	IGCGLLGLPLAVKAGIYMGPIISLLIGVAVHMGILLYKCAAHFCRPLINKSFYDGDY	119						
Qy		121	MYGIESSPESWLRNHAHNGRRVDFFLVTLQGFCVYFVFLADNFQVIEANGTNNC	180						
Ddb		120	MYGIECSPTWIRNLSHNGRRVDFFLVTLQGFCVYFVFLADNFQVIEANGTNNC	179						
Qy		181	HNNETVILTPMDSLRYMLSFPLPVLLVFIIRNLRLSIFSLNANITMLVSLMIVOFIV	240						
Ddb		180	HNNETVILTPMDSLRYMLSFPLPVLLVFIIRNLRLSIFSLNANITMLVSLMIVOFIV	239						
Qy		241	QRIDDPHSLPLVAKWTKPLFFGTAIFPEGIVMLPLENKMDPKRKEPLILYGMIVT	300						
Ddb		240	QRIDDPHSLPLVAKWTKPLFFGTAIFPEGIVMLPLENKMDPKRKEPLILYGMIVT	299						
Qy		301	IILYSLSGCGYLOFGANIGOSITIILNLPNCWLYQSVKLILYSIGIFTYTAQFVPAEIIIP	360						
Ddb		300	IILYSLSGCGYLOFGANIGOSITIILNLPNCWLYQSVKLILYSIGIFTYTAQFVPAEIIIP	359						
Qy		361	FFVYRAPHCEPHCIVVDDLFVTVLCLTCITLALIPLRDLVSYSSSALAIIPPLE	420						

Db	360	AIYRSVPERFLVUDLSARTAMCVTCVLAVLPIRDLVLSVGSVSSALIIPPLLE	419
Qy	421	VTTFYSEGMSPLTIFKDALISILGFVGFVYGTYBALYELIOPSNAPIFINSTCAF1	476
Db	420	VTTYGEGISPLTTKDALISILGFVGFVYTSWELLQPSHSDSSTNSTSAPI	475
RESULT 14			
ABP96443	ABP96443	standard; protein; 475 AA.	
ID	ABP96443		
XX	AC	ABP96443;	
XX	XX	02-JUN-2003 (first entry)	
DT	XX		
DE	XX	Mouse tramordin 3 protein SEQ ID NO:2.	
XX	XX		
KW	XX	Neuroprotective; nootropic; cerebroprotective; analgesic; gene therapy;	
KW	XX	central nervous system disorder; CNS disorder; multiple sclerosis;	
KW	XX	nerve injury; neuropathic pain; stroke; trauma; non-CNS disorder; tramordin; mouse; tramordin 3.	
KW	XX		
OS	OS	Mus sp.	
XX	XX		
PN	PN	W02003016502-A2.	
XX	XX		
PD	PD	27-FEB-2003.	
XX	XX		
PF	PF	21-AUG-2002; 2002WO-US026637.	
XX	XX		
PR	PR	21-AUG-2001; 2001US-0313907P.	
PR	PR	21-AUG-2002; 2002US-00225810.	
XX	XX		
PA	PA	(MCLA-) MCLAHLIN RES INST.	
XX	XX		
PI	PI	Birmingham JR;	
XX	XX		
DR	DR	WPI; 2003-278567/27.	
DR	DR	N-PSDB; AB280238.	
XX	XX		
PT	PT	New nucleic acid sequence encoding tramordin, e.g. mouse tramd 1, mouse tramd 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, or the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1 is located to chromosome 11, whereas human tramd 1 is located to chromosome 5q31-33. The tramd sequences have neuroprotective, nociceptor, analgesic and cerebroprotective activities, and can be used in gene therapy. The nucleic acid sequences are useful for diagnosing and treating central nervous system (CNS) disorders such as multiple sclerosis, nerve injury, neuropathic pain, stroke or trauma, and non-CNS disorders. The present sequence represents mouse tramd 3, which is given in the exemplification of the present invention	
PT	PT		
PT	PT		
XX	XX		
PS	PS	Example 11; Fig 23A; 177pp; English.	
XX	XX		
CC	CC	The present invention describes an isolated nucleic acid sequence comprising a cDNA sequence encoding mouse tramordin (tramd) 2, mouse tramd 3, human tramd 1, human tramd 2, human tramd 3 or rat tramd 1, or the genomic sequence of mouse tramd 1 or mouse tramd 3. Mouse tramd 1 is located to chromosome 11, whereas human tramd 1 is located to chromosome 5q31-33. The tramd sequences have neuroprotective, nociceptor, analgesic and cerebroprotective activities, and can be used in gene therapy. The nucleic acid sequences are useful for diagnosing and treating central nervous system (CNS) disorders such as multiple sclerosis, nerve injury, neuropathic pain, stroke or trauma, and non-CNS disorders. The present sequence represents mouse tramd 3, which is given in the exemplification of the present invention	
CC	CC		
SQ	SQ	Sequence 475 AA;	
Query Match	86.9%	Score 2144.5; DB 6; Length 475;	
Best Local Similarity	86.1%	Pred. No. 1e-222;	
Matches 410;	Conservative	Mismatches 32; Indels 1; Gaps 1	
1	MSTQRURNEDYDYSSTTDVSPEPSSSEGFLNNLSSPGSYQRFQSMSTTWFOTLTHLKG	N 60	
1	MSTQRURNEDYDYSSTTDVSPEPSSSEGFLNNLSSPGSYQRFQSMSTTWFOTLTHLKG	N 59	
Qy	1	IGTGLLGLPLAVKNAIGIVMGPISLLIGIVAHNGILVCKAHHPCRINKSPVFDYGDY	120
Db	60	IGTGLLGLPLAVKNAIGIVMGPISLLIGIVAHNGILVCKAHHPCRINKSPVFDYGDY	119

Qy	121 MYGLESSPCSWLNRNHAHWRGRVVDFFLITVOLGCCVYFVFLADNPKQVIEAANGTTN 180	CC disorders
Db	120 MYGLECSPSTWTRNHSHWGRITVDFFLITVOLGCCVYFVFLADNPKQVIEAANGTTN 179	XX Sequence 475 AA;
Qy	181 HNNETVILTPMDSRMLMSFLPFLYLVFLRNRLAISIFSLANITMVLSSLMIVYQFIV 240	Query Match 86.8%; Score 2142.5; Length 475;
Db	180 NNNNTVVIPTPMDSRMLMSFLPFLYLVFLRNRLAISIFSLANITMVLSSLMIVYQFIV 239	Best Local Similarity 85.5%; Pred. No. 1.7e-222; Mismatches 37; Conservative 31; Indels 1; Gaps 1;
Qy	241 QRIDPSHLPLAPWKTYPLPFGTAFLSSEGIGMVLPLENKMDPKFLPLYLGVNIVT 300	Matches 407;
Db	240 QRIDPSHLPLAPWKTYPLPFGTAFLAPEGIGVVLPLENKMDSKPLYLGVNIAIT 299	1 MSTRQRNEDYHDYSSSTDVSPBESPPBGLNNLSSPSYQRFGQNSSTTWFTQLLHLIKGN 60
Qy	301 ILYISLGCLGYLQGANILOGSTIINLPNCMLYQSVKLILYSIGIFFTYALQFYVPAELIP 360	1 MSTRQRNEDYHDYSSSTDVSPBESPPBGLGSF-SPEGLGSF-SPEGLGSF
Db	300 VLYISLGCLGYLQGANIKGSSTIINLPNCMLYQSVKLILYSIGIFFTYALQFYVAAEIIIP 359	1 MSTRQRNEDYHDYSSSTDVSPBESPPBGLGSF-SPEGLGSF-SPEGLGSF
Qy	361 FFVSRAPHECLVVDLFVRTVFLVCLTCILALIPRLDVLVISLGVSSALALIPLLE 420	121 MYGLESSPCSWLNRNHAHWRGRVVDFFLITVOLGCCVYFVFLADNPKQVIEAANGTTN 180
Db	360 AIVSRVPEHFLMDLCVRTAMVCVTCILALIPRLDVLVISLGVSSALALIPLLE 419	120 MYGLECSPSTWTRNHSHWGRIVDPLFLVQLGFCCCVYFVFLADNPKQVIEAANGTTN 179
Qy	421 VTTFSEGMSPSTIFKDALISLILGFVFGVFTYEALYELIOPSNAPIFINSTCAFI 476	181 HNNETVILTPMDSLYMLSPFLPFLVLSFRNLRLSIFLLANTMVLSSMIVQFIV 240
Db	420 VVTYGBGISPLTVKDALISLILGFVFGVFTYESLCELIOPSHSDSNTNSTSAFI 475	180 NNNETVILTPMDSLYMLSPFLPFLVLSFRNLRLSIFLLANTMVLSSMIVQFIV 239
<hr/>		
RESULT 15		
ID	AB76935 standard; protein; 475 AA.	Qy 301 ILYISLGCLGYLQGANILOGSTIINLPNCMLYQSVKLILYSIGIFFTYALQFYVPAELIP 360
XX		Db 300 VLYISLGCLGYLQGANIKGSSTIINLPNCMLYQSVKLILYSIGIFFTYALQFYVAAEIIIP 359
AC	AB76935;	Qy 361 FFVSRAPHECLVVDLFVRTVFLVCLTCILALIPRLDVLVISLGVSSALALIPLLE 420
XX		Db 360 AIVSRVPEHFLMDLCVRTAMVCVTCILALIPRLDVLVISLGVSSALALIPLLE 419
DT	22-JUL-2002 (first entry)	Qy 421 VTTFSEGMSPSTIFKDALISLILGFVFGVFTYEALYELIOPSNAPIFINSTCAFI 476
DE	Rat VG51.	Db 420 VVTYGBGISPLTVKDALISLILGFVFGVFTYESLCELIOPSHSDSNTNSTSAFI 475
XX	Rat; antiasthmatic; anxiolytic; antiepileptic; antihypertensive; transporter; GABA; neurotransmitter; neurotransmitter; psychiatric disorder; neurotic disorder; VG51.	
XX		Search completed: August 24, 2006, 01:19:44
OS	Rattus sp.	Job time : 196 secs
PN	WO2000071709-A1.	
XX		
PD	30-NOV-2000.	
XX		
PF	19-MAY-2000; 2000WO-FR001383.	
XX		
PR	21-MAY-1999; 99FR-00006525.	
XX		
PA	(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.	
XX		
PI	Giros B, Gasnier B, Sagne C, El Mestikawy S, Hamon M;	
XX		
WPI	2001-025160/03.	
DR	N-PSB; ABL57913.	
XX		
PS	Claim 2; Fig 2; 103pp; French.	
XX		
CC	The present sequence is the protein sequence for rat VG51, a glutamate/	
CC	gamma-aminobutyric acid (GABA) transporter. GABA and glutamate are	
CC	neurotransmitters. The transporter can be used to produce specific	
CC	antibodies, to screen for binding agents. Modulators of the transporter	
CC	are useful for treating disorders associated with deregulated	
CC	Glutamate/GABA transport, e.g. asthma, anxiety, epilepsy, hypertension	
CC	and other psychiatric and neurotic disorders, while determining levels of	
CC	the transporter and its coding sequence can be used for diagnosis of such	

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OM protein - protein search, using sw model

Run on: August 24, 2006, 01:19:59 ; Search time 41 Seconds  
 (without alignments)

1117.053 Million cell updates/sec

Title: US-10-679-362-2

Perfect score: 2469

Sequence: 1 MSTQRRLRNEDYHDYSSSTDVS.....YELIQPSNAPIPINSTCAFI 476

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing First 45 summaries

Database : PIR 80:\*

- 1: Pir1:\*
- 2: Pir2:\*
- 3: Pir3:\*
- 4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1677.5	67.9	481	2 JC7961	----- proton-coupled ami
2	672	27.2	607	2 T26845	hypothetical prote
3	465.5	26.4	449	2 H88022	protein T27A1.5 [i
-4	465.5	18.9	436	2 T05653	amino acid transpo
5	465.5	18.9	713	2 S88251	probable membrane
6	462	18.8	434	2 T15799	hypothetical prote
7	462	18.7	481	2 T23191	hypothetical prote
8	443.5	18.0	460	2 F88544	protein F59B2.2 [i
9	431.5	17.5	467	2 T26705	hypothetical prote
10	415	16.8	656	2 T38741	major facilitator
11	388.5	15.7	692	2 S37976	hypothetical prote
12	368	14.9	389	2 S31123	hypothetical prote
13	285.5	11.6	543	2 T48239	hypothetical prote
14	276	11.2	516	2 T48238	hypothetical prote
15	274.5	11.1	426	2 T51506	hypothetical prote
16	270.5	11.0	529	2 E84813	hypothetical prote
17	263	10.7	503	2 T26524	hypothetical prote
18	259	10.5	890	2 T21000	hypothetical prote
19	251.5	10.2	462	2 S42372	hypothetical prote
20	251.5	10.2	486	2 T42254	amino acid permeas
21	247	10.0	423	2 T49959	hypothetical prote
22	233.5	9.5	571	2 T06737	hypothetical prote
23	233	9.4	484	2 T34016	hypothetical prote
24	232	9.4	509	2 S5413	probable membrane
25	230	9.3	494	2 T6658	hypothetical prote
26	224	9.1	476	2 C96505	probable amino aci
27	222	9.0	505	2 B88206	protein F2D12.3 [
28	215.5	8.7	485	2 A48187	amino acid transpo
29	210	8.5	448	2 S50622	hypothetical prote

## ALIGNMENTS

RESULT 1

JC7961 proton-coupled amino acid transporter 2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Aug-2003 #sequence\_revision 25-Aug-2003 #text\_change 15-Sep-2003

C;Accession: JC7961

R;Chen, Z.; Kennedy, D.J.; Wake, K.A.; Zhuang, L.; Ganapathy, V.; Thwaites, D.T. Biochem. Biophys. Res. Commun. 304, 747-754, 2003

A;Title: Structure, tissue expression pattern, and function of the amino acid transporter

A;Reference number: JC7961; PMID:12727219

A;Accession: JC7961

A;Molecule type: mRNA

A;Residues: 1-481 <CHE>

A;Experimental source: (lung)

C;Comment: This transport protein is a second member of H<sup>+</sup>-coupled, pH-dependent, Na<sup>+</sup>-in sport not only from one cellular compartment to another (across plasma membrane) but also from one compartment to another (across membrane)

C;Genetics:

A;Gene: PAT2

A;Map position: 10q22

C;Keywords: amino acid transport system; PAT2

Query Match 67.9% ; Score 1677.5; Best Local Similarity 71.7%; Pred. No. 2.7e-127; Matches 325; Conservative 54; Mismatches 67; Indels 7; Gaps 1;

Qy 20 SPEESPESEGNNLSSPGSYQRFGQNSNTWFTOLIHLKGKGNITGIGLPLAVKNAIGIVM 79

Db 32 SQDPNVEGNGSSESSSE-----KTKGIGTGTQTLVHLVRKGNGMTGIGLPLAVKNAIGILM 84

Qy 80 GPISLILIGIVAVHNGILVYKRCAHHFCCRRLINKSFVYGDFTVYMGLESSPSCSWLRLNAHVG 139

Db 85 GPLSLIVMGLIATICHMHLIVRKCAQRICHRLINKPFMDYGDFTVYMGLESSPSCSWLRLNAHVG 144

Qy 140 RRVDPFFLIVTQLGFCYYFVFLANFKVIBAANGTNNCNHNNETVILPTMDSRYML 199

Db 145 RHAVSFFLIVTQLGFCYYFVFLANLQKVEAVNSTTISCKHNETVILPTMDSRYML 204

Qy 200 SFLPLFLVLYPIRNLRLSISLNLANITMLVSLMIVYQFIVRIPDPSHLPLVAPNKTYP 259

Db 205 AFLPVGGLYPIRNLRLVLTISLNLANVSMIVLQVYIQQIPDPSOLPLVAVSMKTP 264

Qy 260 LFFGTAIFSPFEGIGAVLPLENKMKDRKFPLIYQGMVIVTLYISLGCLUGYIQLFGANIQ 319

Db 265 LFFGTAIFSPFEGIGAVLPLENKMKDRRFPLISLGMISITLYIAIGALGYLRFDDIK 324

Qy 320 GSITLNLPNCMWLYQSYKLLYSIGIPTYALOFVYPAEIIIPFVSRAPENCELVYDFVR 379

Db 325 ASITLNLPNCMWLYQSYKLLYVGILCLTHALOFVYPAEIIIPBLAVSoySKRMLPVDLSIR 384

Qy 380 TFLVCLTCILAILIPRLDVLVSLVGSVSSSALLALIIPPLLEVTTFYSEGMSPLTIRKDAL 439

Db 385 LALVCVTCMIALILIPRLDVLVSLVGSVSSSALLALIIPPLLEVTTFYSEGMSPLTIRKDAL 444

Qy	440	ISILGFVGVYGVTEALYELIQPSNAPIPINST	472	A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: H88022
Db	445	ISILGFVGVYGVTEALYELIQPSNAPIPINST	477	A;Status: preliminary A;Molecule type: DNA A;Residues: 1-449 <STO> A;Cross-references: UNIPARC:UPI00000747F8 ; GB:chr_II; PIDN:AB71045.1; PII
RESULT 2				
T26845				A;Map position: 2 C;Superfamily: Arabidopsis amino acid transport protein I
Hypothetical protein Y33F4B.7 - Caenorhabditis elegans				Query Match 26.4%; Score 652; DB 2; Length 449;
C;Species: Caenorhabditis elegans				Best Local Similarity 33.0%; Pred. No. 7, 8e-45;
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004				Matches 146; Conservative 101; Missmatches 160; Indels 36; Gaps 7;
R;Matthews, L.				
R;Submitted to the EMBL Data Library, January 1998				
A;Reference number: Z220276				
A;Accession: T26845				Qy 36 GSYQ------RGQNSNTWTFQTLIHLKGNIGTGLGLPLAVKNAGIVMGPISIILI 86
A;Status: preliminary; translated from GB/EMBL/DBJ				Db 19 GSHOPTMGEFAASRVRSERTSDAQLHMKVMMGTMNLSPFLAEHSIGIWGLLILCF 78
A;Residues: 1-607 <WIL>				
A;Cross-references: UNIPROT:045936; UNIPARC:UPI000017BC76; EMBL:AL021481; PIDN:CAA16336.				Qy 87 IGIVAHCMGILVYKCAAHFCRRLANKSFYDYGDTVMYGLLESSPSCSWLRNNAHAWGRRVYDFF 146
A;Experimental source: clone Y43F4B				Db 79 ICLICUYCTROLIIGQHQTIFIREQRDYANTYRASVELGP-AWIRGHGLPKQMVNTN 137
A;Gene: CESP1Y43F4B.7				
A;Introns: 53/3; 80/3; 110/2; 141/2; 169/3; 229/1; 261/3; 300/2; 320/2; 355/3; 377/1; 41				Qy 147 LIVTQLGRCCVYFVPLADNFKQVIEANGTTNNCHNE---TVILTPTMDSRLYMLSL 202
A;Best Local Similarity 27.2%; Score 672; DB 2; Length 607;				Db 138 MFVAQFGCCVYFVEMADNLKQFFD---QTSSTHISQAGWIALLIP----- 181
A;Matches 150; Conservative 95; Missmatches 180; Indels 26; Gaps 7;				Qy 148 LIVTQLGRCCVYFVPLADNFKQVIEANGTTNNCHNE---TVILTPTMDSRLYMLSL 202
Qy 14 YSSTDVSPE----ESPSLNLNLSSPGS--YQRFQGSNSTWTFQTLIHLKGNIGTGL 66				Db 182 --ISALCMTREKLAKAPLAFLAVANFVYIAVAVILADLFLSDWQPLDSLPAFGAVENLPLFF 239
Db 9 YQEFDNNEPAPGDTEVQTRRTNTSEDTSLFQDRLPTENSLTPEQAFHIMVAKMLGTGL 68				Qy 263 GIAIFSEFGIGMVLPLENKMKDPRKFP-----ILYGMVIVTILYLSLGLGLYLOFGANTQ 319
Qy 67 GLPLAVKNAIGVMPISLILIGITIVAHVCMGILVYKCAAHFCRRLANKSFYDYGDTVMYGLS 126				Db 203 PFLVLFVPLFIRNLALSIFSLLLNPSVYFPLVAPWQKTPYFVQRIIDPSHPLPLVAPWQKTPYFVQ 262
Db 69 SLPLAFKHSGLFLGLLTYLICLICLYCRQVVAHFTCNRNRDLIYANIMRGAVEM 128				Qy 204 GTVNFARFGSVAVLPENQMNPHFPTENGVINTSCLIVLTYMVGFFGFLRYGNDIK 299
Qy 127 SPCSWLNRNAHAWGRVVDFPLIVTQLGFCVVYFVPLADNFKQVIEANGTTNNCHNET 186				Db 240 GSYTILNLPNCWLYQSVKELYSIGIFIFTYALQFVPAELIIPFFVSRAPHEHCELVVDLFLVR 379
Db 129 GP-PWIKRNYCFFQLVNVNMFISQLGFCVVYFVPMADNLEDFF-----NNNTS 176				Qy 320 GSTTILNLPNCWLYQSVKELYSIGIFIFTYALQFVPAELIIPFFVSRAPHEHCELVVDLFLVR 379
Qy 187 ILTPPMDSRIVMLSLPFLVYLVPLFIRNLALSIFSLLLNPSVYFPLVAPWQKTPYFVQ 246				Db 300 DTLTLNLQTPQFVQAKYMFVLCLIVLVSPLQFVPMERVEKWKVKEQKEMTYAIR 359
Db 177 I---HLSKAWMMLLIPMLSLCISIRRLSLAPPAMAANVYVYAVVLFPSDLRPI 233				Qy 380 TVLVLVCLCLAILIPRLDIVISVGSVSSSALLIIPPLEVTTFYS-BGMSPLTIFKDA 438
Qy 247 SHLPLVAPWQKTPYPLFFGTAIFSFSEGIGMVLPLENKMKDPRKFP---IILYGMVIVTLY 303				Db 360 FGGVLLTCAQALIPHLLALFISLYGSVAGTSLTFLVFPPLIELLCSYSKOLETKWVWIRNI 419
Db 234 SSLPWFGRATDLPFLGTVMAFFEGVAVMPIMQSSHAFISWNGVUNSSCLIVLIAF 293				Qy 439 LISLGFYGVVCTYEALEYLIQ 461
Qy 304 ISLGCLGYLOFGANIQQSSTIINLPCNCWLYQSVKLILYSGIFFYALQFVPAELIIPFFV 363				Db 420 GLMFAFMGFTGTYASHMVIQIE 442
Db 294 SVTGFYGYLSLGLNDYKDTATLNLPMTFQYKLMFVACIMISYPLQYVPMRERIKWT 353				
Qy 364 SRAPPHCELVWDLFVRTVLCVLTCLLAIIPRLDIVISVGSVSSSALLIIPPLEVTT 423				RESULT 4
Db 354 RKIPFDQKTIYIARYSGVLTCAIELIPHALFISLGAFGASMLLFFCIELT 413				T06653
Qy 424 FYSEG-MSPLTIFKDALISLGFYGVVCTY 453				A;Map position: 4 C;Species: Arabidopsis amino acid transport protein I
Db 414 SYAKNELSTGLWIKNVLTFAPIGFTGTY 444				C;Species: Arabidopsis amino acid transport protein I
Qy 50 FQTLIHLKGNIGTGLGLPLAVKNAGIVMGPISLILGIVAVHCMGILVYKCAHFCRRL 109				A;Note: F22113.20
Db				A;Accession: H88022
R;Anonymous, The C. elegans Sequencing Consortium.				A;Molecule type: DNA
Science 282, 2012-2018, 1998				A;Residues: 1-436 <BEV>
A;Title: Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biological				A;Cross-references: UNIPARC:UPI00000747F8 ; GB:chr_II; PIDN:AB71045.1; PII
A;Reference number: A75000; MUID:99069613; PMID:9851916				A;Experimental source: cultivar Columbia; BAC clone F22113
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg				C;Genetics:
C;Species: Caenorhabditis elegans				A;Map position: 4
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004				A;Note: F22113.20
C;Accession: H88022				
R;Anonymous, The C. elegans Sequencing Consortium.				
Science 282, 2012-2018, 1998				
A;Title: Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biological				
A;Reference number: A75000; MUID:99069613; PMID:9851916				
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg				

Db	37	FTKTFANVPIAVVGAGVGLGLGLYAFKRTGWLNGVLLVSVLTHCMMLVY-----YTRK	91	P:486_502;Domain: transmembrane #status predicted <TM5> P:516_532;Domain: transmembrane #status predicted <TM6>
Qy	110	NKSF-----VGYDTVMYGLLESSPCSNLNRNHAHGRVYDFFLIVTOLGFCCVYFVYI	162	F:557_573;Domain: transmembrane #status predicted <TM7> F:626_642;Domain: transmembrane #status predicted <TM8> F:649_665;Domain: transmembrane #status predicted <TM9> F:689_705;Domain: transmembrane #status predicted <TM10>
Db	92	LDSFNAGISKIGSFGD-----LGFAVCGS-----GRIVDLFILSQAGFCVGLYI	140	
Qy	163	ADNFQVIEANGT-----NNCHNETVLTPT-----MDSPLYMLSLFLPFL	205	Query Match 18.9%; Score 465.5; DB 2; Length 713; Best Local Similarity 31.0%; Pred. No. 1..3e-39; Matches 144; Conservative 81; Mismatches 167; Indels 73; Gaps 18;
Db	141	-----GTTLNLS-----SPTLSRHQFTRLGSEFLGVSSKSLYINGCFFPQ	184	
Qy	206	VLLVFINLNLALSTESLLANI-----TMLVSLVMIQFIVORIPDPSHLPIVAPWKTPFL	261	Qy 32 LSSPGYQRFQSNSTN-WFQTLHILKGNIGTGLGLPLAVKAGNAIVMGPISLLIIGIV 90
Db	185	LGSLISKTLTHLAPISIIFIADLGAMAVTIVEDSMILKQRPD-----VVAEGMSLUF	238	Db 281 LSRPDMKVLPSAKGTISTKRVFLILKSFIGTGVFLPNFAHNGGFFFSVMSLAFFCIY 340
Qy	262	---FGTAIFFSEFGIGMVLPLLENKMDKPRKEPLILYLGIVTILYISLGCGLYQFGANT	318	Qy 91 AVHCMGILVVKCAHHFCRRLNKSFDVYDGTVMYGLLESSPCSWLNRNHAHGRVYDFFLIVT 150
Db	239	LYGMCAVATISSEGVMVNLPLJESEMKDQDKFGLVLAQGLYLAQFGEDT	298	Db 341 SYWCYTYLQV-AKSSCG--VSFGDGG-----LKLGYPMWRLTILFLSLVIT 383
Qy	319	QGSTINLNPNCWLYOSVKLISIGFETYLQFYPAEILIPFFYRAPHCELYVVDLFV	378	Qy 151 QLGFCVCYFVFLADNFKQVIAANGTNNCHNNETVLTPTMDSLRYMLSLFLPFLV-LV 209
Db	299	MDTTANLQAGLVSTVQGLCIN-----PLMMNNVFEITERRF-SRG-----MYSANL	351	Db 384 QVGFSGAYMITAKNQAFLD-----NVFH----YGVLPPLS----YLMVFTQIIFIPLS 429
Qy	379	RTVLYCLTCAILAIPLDVLISLVGSVSSALALIPLPLEVTTFYSSEGMSPLTIFKA	438	Qy 210 FIRNLALSTPSLLANITMLVSLVMMYQFIVQRI-DPPSHPLVVA-----PWTYPL 260
Db	352	RWLVLAATVLVALFVNPNAFLSLSGSSTCCVILGVFLPAFLHLLVVF-KEEMGWLQWSST	410	Db 430 FIRNISKSLSLSSLLANPIMAGLVLVIIIFTAKRLFPLDMGTIPAMGIVYGLNADRW--TL 486
Qy	439	LISLIGFVGFGVGTIBALYL	459	Qy 261 FFGTAAFSPEGIGMVLPLLENKMDKPRKEPLILYLGIVTILYISLGCGLYQGANIQG 320
Db	411	AIWLGVLVLAQSGTWSSLSEI	431	Db 487 FGTATAFEGGGLIPVQDSNRNPXPLPVIAVLTATLFLFISATLGYLAYSNSVQ 546
<b>RESULT 5</b>				
S58251	probable membrane protein YNL101w - yeast (Saccharomyces cerevisiae)			
N;Alternate names:	hypothetical protein N2185			
C;Species:	Saccharomyces cerevisiae			
C;Date:	13-Jan-1996 #sequence revision 23-Feb-1996 #text_change 09-Jul-2004			
R;Saiz, J.E.; Buitrago, M.J.; Soler, A.; del Rey, F.; Revuelta, J.L.	submitted to the EMBL Dalt Library, July 1995			
R;Saiz, J.E.; Buitrago, M.J.; Soler, A.; del Rey, F.; Revuelta, J.L.	submitted to the EMBL Dalt Library, April 1996			
A;Description:	Sequence of a 21.3 kb fragment from the left arm of yeast chromosome X1			
A;Reference number:	S58246			
A;Accession:	S58251			
A;Molecule type:	DNA			
A;Residues:	1-713 <SAW>			
A;Cross-references:	UNIPROT:P50944; UNIPARC:UPI0000052B6D; EMBL:Z50161; PID:g929846; PID:CAA95977.1; F			
R;Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, J.L.	Submitted to the Protein Sequence Database, April 1996			
A;Reference number:	S63037			
A;Molecule type:	DNA			
A;Residues:	1-713 <SAW>			
A;Cross-references:	UNIPARC:UPI0000052B6D; EMBL:Z71377; PID:g1302013; PID:CAA95977.1; F			
R;Saiz, J.E.; Buitrago, M.J.; Soler-Mira, A.; del Rey, F.; Revuelta, J.L.	Yeast 12, 403-409, 1996			
A;Title:	The sequence of a 21.3 kb DNA fragment from the left arm of yeast chromosome X1			
A;Reference number:	S63038; MUID:96267765; PMID:8701612			
A;Accession:	S63053			
A;Status:	nucleic acid sequence not shown			
A;Molecule type:	DNA			
A;Residues:	1-713 <SAF>			
A;Cross-references:	UNIPARC:UPI0000052B6D; EMBL:Z50161; PID:g929846; PID:CAA90525.1; PI			
C;Genetics:	SGD:S0005045			
A;Cross-position:	141			
A;Note:	YNL101w			
C;Superfamily:	Saccharomyces cerevisiae probable membrane protein YNL101w			
C;Keywords:	Saccharomyces cerevisiae protein			
F:312_318;Domain:	transmembrane #status predicted <TM1>			
F:314_390;Domain:	transmembrane #status predicted <TM2>			
F:412_466;Domain:	transmembrane #status predicted <TM3>			
F:442_458;Domain:	transmembrane #status predicted <TM4>			
<b>RESULT 6</b>				
T15799	hypothetical protein C44B7.6 - <i>Caenorhabditis elegans</i>			
C;Species:	<i>Caenorhabditis elegans</i>			
C;Date:	20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004			
R;Du, Z.				
A;Description:	submitted to the EMBL Data Library, June 1995			
A;Reference number:	S61146			
A;Accession:	T15799			
A;Molecule type:	DNA			
A;Residues:	1-713 <SAW>			
A;Cross-references:	UNIPROT:Q18595; UNIPARC:UPI000017B834; EMBL:U28928; NID:986			
C;Genetics:	CESP:C44B7.6			
A;Gene:	CESP			
A;Introns:	22/2; 52/3; 82/2; 113/2; 141/3; 195/3; 250/1; 293/2; 356/1			
Qy	LHLLIKNCIGTGLGLPLAVKAGNIVMGPISLLIIGIVAHVNGILYCAHHFCRIRNKS 112			
Db	27 LINLMKMLGAGCFSPVLAFKOSGYVSGLVIIVLGFICALCMVLYCAGLKVNSQSA 86			
Qy	113 FVDYGDYTMYGLLESSPCSWLNRNHAHGRVYDFFLIVTOLGFCCVYFVYI 172			

Db	87 PLDGN-MAYKATASYTPPIRKLAPEVSLAVNSSLCLLGICCFYFVVTHLHELLE 145	Qy	406 VSSSALLALIIPPLEVITIIFYSEGMSPLTIFK-----DALISILGFVGFVVG 451			
Qy	173 ANGTTNNCHNETVILTPMDRLYMLSSPLFLVLFTRNLRLSIFSLLANITMLVSL 232	Db	416 TSGDLISLILPSFLDCMVF-----LDFVKRQGDMFKPYQKLLINVELFVLSWFLGAG 468			
Db	146 ---YVANDVPSRAT-LFPNV-----LPAFLVLSISSLRSLVSGNPLMLIAL 191	Qy	452 TYEALYEI 460			
Qy	233 VMIYOFIVQRIQDPS-HLPIVAPWKTYPPFFGTAIFSEFGKMYPLENKMDPFR--KFP 289	Db	469 LVISSDDII 477			
Db	192 AVIMFQOLLTEHKKLADLPEVTDLGMIVSAACTYALEQAMVPLERNMKKPEDMKGP 251	RESULT 8				
Qy	290 L-ILYLGMYWVTTILYISLGLCLGYLQSGNQIYQSVKLWYSGKFL 348	Qy	protein F88B2.2 [Imported] - Caenorhabditis elegans			
Db	252 FGVLISVGVRGVNIVVYISFAGFFGFLTYGNDQDSITLNLENDHGLIFKVAVLFLVYSSFL 311	C;Species: Caenorhabditis elegans				
Qy	349 LQFVYPAELIIPFFVSRAPHEH-----ELVVDLFVTRTLYCILCTCILALIPLRDLVSL 402	C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004				
Db	312 IQVPIVAMWPAIKKKURTTGCVSTTRKHFAFRTSIVIVFLSYAIPRLSDMVPFL 371	C;Accession: F88B2.4				
Qy	403 VGSVSSAAALIIPPLEVTTFSBGMSPALTIKFDALISILGFVGFVNGTYEALY 457	Science 282, 2012-2018, 1998				
Qy	372 VGVTAGMILALVLFVPSLFLHLLFLPQEFCRIGFLFEDI--FLDFVCILIGMFVVY 423	A;Reference number: A75000; MUID: 99099613; PMID: 9851916				
Db	A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/					
A;Accession: F88B44						
A;Status: preliminary						
A;Molecule type: DNA						
A;Residues: 1-460 <STOP>						
A;Cross-references: UNIPROT:P34479; UNIPARC:UPI000013B9DA; GB:chr_III; PIDN:CAA77582.1; E						
P88B2.4						
C;Genetics:						
A;Gene: F59B2.2						
A;Map Position: 3						
RESULT 7						
T23131						
C;Species: Caenorhabditis elegans						
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004						
R;Wallis, J.						
submitted to the EMBL Data Library, June 1997						
A;Accession number: Z19691						
A;Accession: T23131						
A;Status: preliminary; translated from GB/EMBL/DBJ						
A;Molecule type: DNA						
A;Residues: 1-481 <WIL>						
A;Cross-references: UNIPROT:062286; UNIPARC:UPI000007809E; EMBL:Z97191; PIDN:CAB10025.1; C;Superfamily: Arabidopsis amino acid transport protein 1						
C;Experimental source: clone H32K16						
C;Genetics:						
A;Gene: CESP_H32K16.1						
A;Map position: 1						
A;Introns: 64/2; 94/3; 124/2; 155/2; 183/3; 337/2; 397/1; 444/2						
C;Superfamily: Arabidopsis amino acid transport protein 1						
Query Match 18.7% Score 462.5; DB 2; Length 481;						
Best Local Similarity 28.7%; Pred. No. 1.5e-29; Mismatches 91; Indels 174; Gaps 8;						
Matches 123; Conservative						
Qy	53 LIHLKGNICTGGLGPIPLAKVNAIGLVMGPISSLILIGIVAHVHCMGLIVKCAHHFCRRLANKS 112	Qy	182 NNETVILTPMDRLSRVLYMSFLPFLVLYFIRNLRLSIFSLLANIITMLVSLVMIQYFIVQ 241			
Db	69 LINFIGMIGPGCFSLAVSKAOGIWMGGIQLALVFLVGFSLSSKMEKIVNCQYLAKSNCIDQ 128	Db	168 RHOQMIMATVVS-----LFLFLTMNFTMRIVSFLVYQYAAVIMQYIVQ 219			
Qy	113 FVDYCGDTVNYGLESSPCSWLNRNHAWGRRVDFELVTOLGFCVCFYFVFLADNFKQVTEA 172	Qy	242 RIPPSPHFLPVAWPRTPLFFGTAIFSEPGIWMPLLENKMDPFRKF--PL-LILGMV 298			
Db	129 SLIDGEMAAZAMQNS-YKMARXKGKLAIVINACILAFQLGIVTIVMFPAEVHIEIWF 187	Db	220 QPNQWDKLPAAATNTFTGTTMIGNSMAYAEGQTMILPIENKLDPAAFLAPFGVLSSTM 279			
Qy	173 ANGTTNNCHNETVILTPMDRLYMLSSPLFLVLFTRNLRLSIFSLLANITMLVSL 232	Qy	299 VTVLISLICLGLYIQLGANIQTSITLNLPNCWLYQSVKLWYSGKFLVYQFVPAEII 358			
Db	188 FADSP-----PPFSKCVMLMYPV-PQMLNFP-GHMKLTLLFGNVIIFAAI 235	Db	280 CTATMFTAGFFGFTGFGDIAPIFTVNPKEGLITVNPMLQSLLGSIAIMVYDPM 339			
Qy	233 VMIYOFIVQRIQDPS-HLPIVAPWKTYPPFFGTAIFSEFGKMYPLENKMDPFRKF-- 288	Qy	359 I----PFFVSRAPHECIELVVDLFLVCLTLLIPLRDLVIVSLVGSVSSSALI 414			
Db	236 VLIITKELMWTWTPWELGSGVGTGEGISAAAGALYSPFGQAMVLPMENSLKVPKDMTC 295	Db	340 ENGRFRKEGARFPVPKWNLSDKGFRFVFLVTVLMAVLPKLEIMPLVGVTSSALCALI 399			
Qy	289 PLILYGLMVWVTTILYISLGLGYLOGANIQTSITLNLPNCWLYQSVKLWYSGKFLVYQFVPAEII 348	Qy	415 IPLLVEITFYSKEMSPLT-----IFKDALLISILGFVGFVNGTYEALYELIQSNAP 466			
Db	295 TGVLSSTAMNLVTVLYAFLGEGFYYTFGPAVQGSLTLLNLSLTVSKGLVKKFGSA 355	Db	400 FPPPFEMITFWTDWKGLLTYRORMTKIFINLVMAIGVFAIACTVNTIHAIQSFSQP 458			
RESULT 9						
T26705						
hypothetical protein Y38H6C.17 - Caenorhabditis elegans						
C;Species: Caenorhabditis elegans						
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004						
C;Accession: T26705						

R; White, S.  
Submitted to the EMBL Data Library, September 1998  
A; Reference number: Z20255  
A; Accession: T26705  
A; Status: preliminary; translated from GB/EMBL/DBDJ  
A; Molecule type: DNA  
A; Residues: 1-467 <WIL>  
A; Cross-references: UNIPROT:Q9XX44; UNIPARC:UPI000006128F; EMBL:AL031630; PIDN:CAA20995.  
A; Experimental source: clone Y38H6C  
C; Genetics:  
A; Map position: 5  
A; Introns: 9/2; 49/2; 79/3; 109/2; 140/2; 168/3; 225/3; 322/2; 382/1; 429/2  
C; Superfamily: Arabidopsis amino acid transport protein I

Query Match 16 8%; Score 415; DB 2; Length 656;  
Best Local Similarity 29 4%; Pred. No. 1.4e-25;  
Matches 125; Conservative 84; Mismatches 168; Indels 48; Gaps 12;

Qy 8 NEDYHDYS-STDVSSP---EESPSEGANNLSSPGSYORFGOSNSTTWFOTLILKGNIG 62  
Db 232 DEDDTDFAMPDVNPNSLHSTVPSQEPLISRHGRTKLQTPGNAANGKAVIL-LILKSFGV 290  
Qy 63 TGLLGIPLAKVAGITVNGPISLLIGIVAHCMGILVKCAHHFCRRLNKSFDYGDPTVMY 122  
Db 291 TGVLFITPKAKFLGGLVFSSATLILGVLSHICFLILLQTR--MKVPGSGFDIGGT-LY 345  
Qy 123 GLESPSPCSWLRNHAIWGRVYDFELVTOLGFCCTYFVELADNFKQVTEANGTNNCHN 182  
Db 346 G-----PRM-RFAILASLTVSQGFSAYISVASTLQACVK----- 381

Query Match 17 5%; Score 431 5; DB 2; Length 467;  
Best Local Similarity 26.8%; Pred. No. 4.4e-27;  
Matches 116; Conservative 98; Mismatches 180; Indels 39; Gaps 8;

Qy 53 LIHLKGNIGTGLGLPLAKVAGITVNGPISLLIGIVAHCMGILVKCAHHFCRRLNKS 112  
Db 54 LINFVGMMGPGCFSLAVSFQAGLWGGFASVFLIGGLSLSYSMHKLIVNCQFSLSERKGDDQ 113  
Qy 113 FVDYGDITVMYGLESSPWLNNHAHGRVVDFFLIVTOLGFCCYYFVELADNFKQVIEA 172  
Db 114 KLDYGMKAMS- -YGAWAKKYGIAKAKVONTCLIAFLQGLVITYSMIFAVEHIEIWQF 172

Qy 173 ANGTTNNCHNETVLTPTMSRSLYMLSFELFLVILVIRNRLSISFLSLANTIMLVS 232  
Db 173 IAGSP-----PFSKIVLVLIMYFV- QMFLNLGHIRITFLSICGNVIIFAAI 220

Qy 233 VNIYQFIVQRIPDPS-HLPVAPVKTPLPFGTAIFSEFEGMVLPELNKMKDP--RKF 288  
Db 221 ALITQELISHFWPYWPTELPSITGVEGVSLAAGSLIYSEFGAMVPLPELNKSHKPQDMRGL 280

Qy 289 PLIYLGMVITVILYTSGLGCLGYLQFGANTQSITINLNPNCWLYCOSVKKLYSIGIFTY 348  
Db 281 TGVLSIAMNVIVFVYAFGLFFGYIAFGPDVRSGLTUNLNPNSVLSVTKGLLKVLGNA 340

Qy 349 LQFYPAEITLIPPFVSRAPERCFLVDF---VRTVFLCCTCLLALIPRLDVISLVGS 405  
Db 341 LQLFLITVQMLPSLQAKVSENKRKLHKLIPYALRSLMVLSSLALAVPNITEIIPFGVGI 400

Qy 406 VSSSALALIIPPLLEVTF-----YSBMSPLTIFKDALISLILGFVGEVGT 452  
Db 401 TSGLLISLIIISFLDCITVFLPKLGERKEKNYYQRMNTIVIF----VLGWLILGSGL 454

Qy - 453 YEALYELIOPNSA 465  
Db 455 YSSIDDVINNNDS 467

RESULT 10  
T38741 major facilitator protein homolog - fission yeast (Schizosaccharomyces pombe)  
C; Species: Schizosaccharomyces pombe  
C; Accession: T38741  
C; Date: 03-Dec-1999 #text\_change 09-Jul-2004  
R; Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.  
submitted to the EMBL Data Library, September 1995  
A; Reference number: Z21808  
A; Accession: T38741  
A; Status: preliminary; translated from GB/EMBL/DBDJ  
A; Molecule type: DNA  
A; Residues: 1-656 <GEN>  
A; Cross-references: UNIPROT:Q10074; UNIPARC:UPI000013A128; EMBL:Z68144; PIDN:CAA92262.1;  
A; Experimental source: strain 972h-; cosmid c3H1  
C; Genetics:  
A; Gene: SPDB:SPAC3H1\_09C  
A; Map position: 1  
A; Introns: 299/2; 361/3; 593/2  
C; Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w

Query Match 16 8%; Score 415; DB 2; Length 656;  
Best Local Similarity 29 4%; Pred. No. 1.4e-25;  
Matches 125; Conservative 84; Mismatches 168; Indels 48; Gaps 12;

Qy 8 NEDYHDYS-STDVSSP---EESPSEGANNLSSPGSYORFGOSNSTTWFOTLILKGNIG 62  
Db 232 DEDDTDFAMPDVNPNSLHSTVPSQEPLISRHGRTKLQTPGNAANGKAVIL-LILKSFGV 290  
Qy 63 TGLLGIPLAKVAGITVNGPISLLIGIVAHCMGILVKCAHHFCRRLNKSFDYGDPTVMY 122  
Db 291 TGVLFITPKAKFLGGLVFSSATLILGVLSHICFLILLQTR--MKVPGSGFDIGGT-LY 345  
Qy 123 GLESPSPCSWLRNHAIWGRVYDFELVTOLGFCCTYFVELADNFKQVTEANGTNNCHN 182  
Db 346 G-----PRM-RFAILASLTVSQGFSAYISVASTLQACVK----- 381

Query Match 183 NETVILPTMDSRILYMLSFELPLFLVIL-IVFIRNLRLSISFLSLANTIMLVS 240  
Best Local Similarity 26.8%; Pred. No. 4.4e-27;  
Matches 116; Conservative 98; Mismatches 180; Indels 39; Gaps 8;

Qy 382 ---VLTSTTHREYHLAVFIFQFLVVPFLSLVTKSISLATSALIAVFLGILLYFWD 438

Qy 241 QRIPPDSHPLPLVAPWNT-YPLFFGTAIFSEFEGMVLPELNKMKDPKRFPLILYLGNNV 299  
Db 439 ITLATKGIAVDAMFNTKTDLSIFLFIGVIAFIFTEGICLILPQEQMAKPNLPLKLTGTMMAI 498

Qy 300 TILYSLGCLGYLQFGANTQSITINLNPNCWLYCOSVKKLYSIGIFTYALQFYVPAEIII 359  
Db 499 SLLFISIGLSSYAAFSKVKVTVVILNPMSPESTTVIQFLVIAILISTPLQFLPATAIE 558

Qy 360 PPFVSRAPERCFLVDFLFLVFLCCTCLLALIPRLDVISLVGS 414  
Db 559 QGIFTFSKERNRKI--KWRKRNLYRLVILVILAILISWAGSSRLFLFYSMVGSVCCPLIYM 616

Qy 415 IPPL 419  
Db 617 YPPML 621

Qy S37976 hypothetical protein YKL146W - yeast (Saccharomyces cerevisiae)  
C; Species: hypothetical protein YKL600  
C; Species: Saccharomyces cerevisiae  
C; Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004  
C; Accession: S37976; S37975; S37805; S44582  
R; Vandembol, M.; Boile, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the Protein Sequence Database, March 1994  
A; Reference number: S37976  
A; Accession: S37976  
A; Molecule type: DNA  
A; Residues: 1-652 <VAN>  
A; Cross-references: UNIPROT:P36062; UNIPARC:UPI000013B735; EMBL:228146; PIDN:9486250; PID  
R; Ramezani Rad, M.; Xu, G.; Kirch Rath, L.; Fritz, C.; Keuchel, H.; Hollenberg, C.P.  
submitted to the Protein Sequence Database, March 1994  
A; Reference number: S37975  
A; Accession: S37975  
A; Molecule type: DNA  
A; Residues: 447-692 <RAM>  
A; Cross-references: UNIPARC:UPI0000178805; EMBL:228146; MIPs:YKL146W  
R; Vandembol, M.; Boile, P.; Dion, C.; Portetelle, D.; Hilger, F.  
submitted to the EMBL Data Library, September 1993  
A; Description: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci  
A; Reference number: S37766  
A; Accession: S37766  
A; Molecule type: DNA  
A; Residues: 1-652 <VAN>  
A; Cross-references: UNIPROT:P36062; UNIPARC:UPI0000168BC6; EMBL:226877; PIDN:9407482; PIDN:CAA81508.1; PI  
R; Vandembol, M.; Boile, P.A.; Dion, C.; Portetelle, D.; Hilger, F.  
Yeast 10, 35-40, 1994  
A; Title: DNA sequencing of a 36.2 kb fragment located between the FAS1 and LAP4 loci  
A; Reference number: S44563  
A; Accession: S44582

A; Status: nucleic acid sequence not shown; translation not shown  
 A; Molecule type: DNA  
 A; Residues: 1-132 <VA3>  
 A; Cross-references: UNIPARC:UPI000016BBC6; EMBL:Z26877; NID:g407482; PIDN:CAA81508; PID:91  
 A; Experimental source: strain S28C  
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993  
 C; Genetics:  
 A; Cross-references: SGD:S0001629  
 A; Map position: 111  
 C; Superfamily: Saccharomyces cerevisiae probable membrane protein YNL101w  
 C; Keywords: transmembrane protein

Query Match 15.7%; Score 388.5; DB 2; Length 92;  
 Best Local Similarity 28.9%; Pred. No. 1.9e-23;  
 Matches 131; Conservative 76; Mismatches 191; Indels 53; Gaps 14;

Qy 8 NEDYHDYSSSTDVSDEESPESEGMLNLSSPSSYQRFQGSNSTTWFQTLIHLIKGNIGTGLG 67  
 Db 260 SEEEEEEETEEEEEPEEALETESTOLVSRSEHGRPHKSKSTV-KAVLILKSPVGTGWF 317  
 Qy - 68 LPLAVKNAQGIVMGPISSLTIGIVAVHCMGLVCKAHHFCCRLLNSFV-YGD-TWYKG 124  
 Db 318 LPKAFAHNGGGWGFSGSALCLLSCALISYGCFSPLITK-----DKVGDYGDGRILYGP 370

RESULT 13

Qy - 125 ESSPCSWLNRHAWHNGRRVYDFFLIVTQGFCCVYFVFLADNFKQVIEAANGTNNCHNNE 184  
 Db 371 KM-----KFAISSLTAAISQIGSAATTVFTATNLQFSE-----NFFH---- 408  
 Qy 185 TVIITP-TMDSRLYMLSPFLPFLVLFIRNLRLAISISSLANITMLVSLVMIYQFIVORI 243  
 Db 409 --LKGPSISLATTYIFAAQVLFVPLSLTRNIAKLSGTALIADLFLIGLIVVYVYVSYIY 465

Qy 244 -----PDPSPHLPLVAPWTPYPLPFGTATTSFQGKPLNLSPFLNPKDPRKFLYLQMV 297  
 Db 466 AVNGYASDTMLMENKADWS--LFGTGTAAFFEGFGLLPIQESMKHPHERPSLSAMC 522  
 Qy 298 IVTLYISLGCLGVIQFGANIQGSITLNLPNCMLYQ-SYKLLYSIGIPTTYALQFYVPAE 356  
 Db 523 IIVAVIFISCCDLCTAAGFSDVYKTVNLNPQDTSTLTLQLLAIIILSTPLQLFPAIR 582

Qy 357 IIIPF-FVSRAPAECELVDL--FVRLTIVCLTCA-ILIPRDLVLSVGSVSSAA 411  
 Db 583 ILENNTTPSNASGKYNPKVWLKNYFRCALVLTSLAVNGANDLKEFVSLVSSFACIPL 642

Qy 412 ALITPPLIETTFFYSEGMMSPLTIFDADLSTLG 444  
 Db 643 YYIYPLLHYKASILSGTSRARLLDILIVVFG 675

RESULT 12  
 S31123 hypothetical protein F59B2.2 - Caenorhabditis elegans  
 C; Species: Caenorhabditis elegans  
 C; Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C; Accession: S31123  
 R; Sulston, J.; Du, Z.; Thomas, K.; Wilson, R.; Halloran, N.; Hawkins, T.; Ainscough, R.; Waterston, R.  
 A; Description: The C. elegans sequencing project: A beginning.  
 A; Reference: S31122  
 A; Status: preliminary  
 A; Molecule type: DNA  
 A; Residues: 1-389 <SUL>  
 A; Cross-references: UNIPROT:P34479; UNIPARC:UPI000017BAS0; EMBL:Z11505; NID:96718; PID:9

Qy 14.9%; Score 368; DB 2; Length 389;  
 Best Local Similarity 28.5%; Pred. No. 4.7e-22;  
 Matches 97; Conservative 72; Mismatches 141; Indels 30; Gaps 7;  
 A; Introns: 387/2; 59/2; 148/2; 343/3

Db 60 YFVNNTILFYQLGMCSTAILVNLVGDHLLGGT---RHOQMLMATVS----- 108  
 Qy 201 FLPFLVLFIRNLRLAISISSLANITMLVSLVMIYQFIVORIIPDSPLSHPLVAPWTKYPL 260  
 Db 109 -LFFILLTNNMFMEMRITVFFALVSSVFFVIGAVIMQYTQOBNQWDKLPAATNTGTIT 167  
 Qy 261 FFGTAIIFSSEGIGMVLPLENKNKDPRKF--PL-ILVGMVITYLISLGCLGIVLQFGAN 317  
 Db 168 MIGMSMATAFEGQMLPENKLDPNAAFLPAPCFLVLSMIICTAFAITALGFFSYTGFDSDS 227  
 Qy 318 IGSSTINLPNCMLYQSYKVLNLSSIGIPTTYALQFYVPAEIII---PFFVSRAPEHCLV 373  
 Db 228 IATITINVPKEGLYSTVNLMLQSLIGNSIAMYYVYDMFFNGERFRKGARPNVPKWL 287  
 Qy 374 VDLFLFVRTLVCLTCILAIATLIPRLDVLVISLGGSVSSAALIIPPLLEVTTFYSEGMSPLT 433  
 Db 288 SDKGFRVFWLVLVLYMAVLPKEIMPLVGTVTSGLCALIIFPPFEMITFWTDWKGLLT 347  
 Qy 434 -----1FKDALISLIGFVGFWVGTQEALYELIQPSNAP 466  
 Db 348 YRQRMTKIFINLIVVMAIGVFAITAGVYTNIATIQSFSQP 387

Query Match 11.6%; Score 285.5; DB 2; Length 543;  
 Best Local Similarity 25.3%; Pred. No. 2.9e-15;  
 Matches 123; Conservative 85; Mismatches 183; Indels 95; Gaps 21;

Qy 2 STQRNRNDYHDYSST--DVSPEEPSGSLNNLSSPGSYQRFQGSNSTWFTOTLHLKLG 59  
 Db 119 SSKPLSOPVDPDKETITLPVNPSQKLUSVTDPLP-----EPNLCSFSQSVLNGTNV 171  
 Qy 60 NIGTGLLGPPLAVKAGIVMGPISSLIGLIVVAVHCMGLVVKCAHFCRRLINKS---FV 114  
 Db 172 LCGLGLITMPYAKESGNGLPI-LFFCIVTCY-TGVLMK---RCLESSPGIQYTP 223  
 Qy 115 DYGDTVMYGLLESSPFCWSLNRNHAHWRGRRVVDFFLITVQLGFCCYVFVLAQN-----FKQV- 169  
 Db 224 DIGAA-FGIDTSSI-----RGVVP-----CVEYIMMSDNLGLFPNVS 262  
 Qy 170 IEAANGTINNNCHNNEVILTPMTDSRLYMLSFLLPFLVLFIRNLRLSIFS---LLANI 226  
 Db 263 LSASGIS-----LDSPQIFAIILTLVLP-----TVWLQDLSLUSYLSVGGLASI 309  
 Qy 227 TMLVSLVMIYQ-----FIVQRIIPDSPLSHPLVAPWTKYPLFFGTAIIFSEFGIGMVLPLEN 280  
 Db 310 LLGICLFWGAVDGIIGFHATGRFVFLSNLPVT-----IGIFGFYGSYHSPNITYS 360  
 Qy 281 KMDKDRPKFPLILYGGMVITLVLISLGCLGIVLQFGANIQGTSITLNLPNCWLYQSVKLLV 340  
 Db 361 SMKDPDSRPLVLFVICSFCTVLYIAVAVGTYMEAVEQSQTFLNMPKHEFFPSKVAWTA 420

Qy 145 FFLIVT---QLGFCCVYFYFLADNFKQVIEAANGTNNCHNNEVILTPMDSRLYMS 200

hypothetical protein FSE19\_80 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: T51506  
 R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asanizu, E.; Kotani, H.; Tabata submitted to the Protein Sequence Database, August 2000  
 A:Reference number: Z55394  
 A:Accession: T51506  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-426 <SAT>  
 A:Experimental source: cultivar Columbia; BAC clone FSE19  
 C:Genetics:  
 A:Map Position: 5  
 A:Introns: 48/1; 247/3  
 A:Note: FSE19\_80  
 C:Superfamily: Arabidopsis amino acid transport protein I  
 Query Match 11.1%; Score 274.5; DB 2; Length 426;  
 Best Local Similarity 25.9%; Prod. No. 1.7e-14;  
 Matches 112; Conservative 80; Mismatches 182; Indels 59; Gaps 15;  
 Oy 44 SNSTTWFOTLILHKGNITGLGLPLAVKNAGIIVMGPISLLITGIVAHCMGILVICKAH 103  
 Db 30 SENNSFLHSVNNNGMLGLQISMPYAVESGG-WMSIPLLISFGILTYTSHILGKCR 88  
 Qy 104 HFCRRLNKSFDVGDYDGVYDFFLITQLGFFCCVYFVFLA 163  
 Db 164 DNFKQVIEANGITNCHNETVILTPMDSLYMLSPFLVLFIRNL-RALSISPS 221  
 Qy 133 DN---ISAAFPATPSNHGH-----FPAAKLTAVAVIALPSLWIRDLSST 175  
 Db 222 LLANITMVLSLV---MIXQFTYORIPDPDPLVAPMKTYPFLFFGTAIFSFSEGIVMLP 277  
 Qy 176 FLSSGGILMSAIIFGSVVYTAFFGGVTDGGKIP-VLRLNIPTVGIVLFSFGG-HIVFP 233  
 Db 278 -LENMKDPRKFPLILYLGMIYVITLISLGCLGLYQFGANIQGSIITLNPNCWLYQSVK 336  
 Qy 234 NLYTSMKDKPSKTFKSVTSFATVYALGAAITGAKMGPSPNQSQTISLPKHLVVTKIA 293  
 Db 337 LLVYSGIFFT-YALQF---YVPAEIIIPPFVSPAPHECBLVVDLFVRLTCLTILAIL 392  
 Qy 294 LWATVLTPTMKVYALEFPLAIIQERSLPLP---STMTRTKVARGLGMGSALLVILALALT 350  
 Db 393 IPRIDLVTSVGSVSSAALIIPPLIEVTTFYS---EGMSPLTIFKDALISLGFYGF 448  
 Qy 351 VPYFGVNLSTGSLSVSVTIAVTLP---SAFYLKICWDMTRKTRAANLGFVVLGVLG 405  
 Qy 449 VVGTTEAUYELIQ 461  
 Db 406 VLGSEFESSKLLVK 418  
 Search completed: August 24, 2006, 01:25:39  
 Job time : 43 secs

RESULT 14

hypothetical protein T7H20\_220 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Accession: T7H20\_220 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Superfamily: Arabidopsis amino acid transport protein I  
 Submitted to the Protein Sequence Database, March 2000  
 A:Reference number: Z24488  
 A:Accession: T48238  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-516 <BEV>  
 A:Cross-references: UNIPROT:O9LZL5; UNIPARC:UPI0000048ABL; EMBL:AL162508  
 A:Experimental source: cultivar Columbia; BAC clone T7H20  
 C:Genetics:  
 Query Match 5%; Score 276; DB 2;  
 Best Local Similarity 24.3%; Prod. No. 1.6e-14;  
 Matches 114; Conservative 82; Mismatches 201; Indels 72; Gaps 15;  
 Qy 10 DYHDYSSTDYSPERSPSEGIVNLSSPQGTYQRFQGSNSTTWFQTLILHKGNITGLGLP 69  
 Db 98 DKDEIQSSVSSSIKSFLASHHQLQSVPGDQDLPQENRSCFSQSVLNGINVLCVALLTMP 157  
 Qy 70 LAVRNAGITMGPISLILIGIVAHCMGILVCKAHFPCRLLNKSTVDFGTVMGLESSP 129  
 Db 158 YAVREGG-WIGLFILESGFSLFTYFTGILKRC-----LENSP- 193  
 Qy 130 SWLNRAHAWHGRVRYDFELVTLQGFFCCVYFVFLADNFKQVIEANGITNCHNETVIL 189  
 Db 194 -GIHTYPDQQAARFTGRLVSAASCVETIMMSDNLSMPNTSLYINGFSLSTQVFA 252  
 Qy 190 PTMDSRLYMLSLFPLPVLLVFPVIRNRLSIFSLLANI--TMLYSLVMIYOFIVORIP-- 244  
 Db 253 ITTT-----LIVLPTVW-LKDLISLSVLSGVISILLALCLFAGSYDGVGPHI 300  
 Qy 245 -----DPSHAPLPLVAPWKTYPLFFGTAIFSPEGIGMVLPLENRMDPDKPXPPLILYLGIVI 298  
 Db 301 SGQALDITNIPVA-----1GIYGF-GSHSVFNPYIYSSMKEPSPPTVLLISFAP 350  
 Qy 299 VTLIYISGCGLGVYQFGANIQGSIITLNPNCWLYQSVKLLYQSGICIFT-YALQF---YVP 354  
 Db 351 CTLFVIAVAVCGFTMFGDIAQSQFTLNMPHFTSKIAVWATVTPMTPXALITTPVNLIS 410  
 Qy 355 AEIIIPFFYSEGMSPLTFKDA---LISLGFGVFGVYEAFLYELI 414  
 Db 411 LEELIP---SSSRKMRSKGSMLFPTILVSLTVNALTVPEFAVAAJGSEFLMLTAI 467  
 Qy 415 IPPLIEVTTFYSSEGMSPLTFKDA---LISLGFGVFGVYEAFLYELI 460  
 Db 456 EPCDCYVTSWCP-----TNTPTQTCIWTIYVWSVSCCCTVYI 512

RESULT 15

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Copyright (c) 1993 - 2006 Biocelleration Ltd.	GenCore version 5.1.9	Q8n856 HUMAN	369	2
OM protein - protein search, using sw model		Q8bubo MOUSE	369	2
Run on:	August 24, 2006, 01:16:39 ; Search time 303 Seconds (without alignments)	Q8msr2 drosophila	369	2
Title:	US-10-679-362-2	Q9v1m3 drosophila	369	2
Perfect score:	2469	Q7kt11 drosophila	369	2
Sequence:	1 MSTQRRLRNEDHYSSSTDVS.....YELIOPSNAPIFINSTCAFI 476	Q9vlm4 drosophila	369	2
Scoring table:	BLOSUM62	Q7q4m8 anophelis g	369	2
GapP:	10.0 , Gapext 0.5	Q5f228 mus musculu	369	2
Searched:	2849598 seqs, 925015592 residues	Q7qfg5 anophelis g	369	2
Total number of hits satisfying chosen parameters:	2849598	Q7pm43 anophelis g	369	2
Minimum DB seq length: 0		Q7pm43 ANOGA	369	2
Maximum DB seq length: 2000000000		Q495m6 HUMAN	369	2
Post-processing: Minimum Match 10%		Q7q19g ANOGA	369	2
Maximum Match 100%		Q8mu61 acyrthosiph	369	2
Listing first 45 summaries		Q9vx84 drosophila	369	2
Database :	UniProt 7.2: 1: uniprot_sprot: 2: uniprot_trembl: *			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	Query Match	Length	DB ID
*	1	24.69	100	0 S36A1 HUMAN
	2	24.39	98.8	476 1 Q4r7m7_MACBFA
	3	23.11	93.9	475 2 Q2VPS4_RAB7A
	4	21.46	86.5	475 1 S36A1_RAT
	5	21.41	86.7	475 1 S36A1_MOUSE
	6	21.41	86.7	475 2 QSF227_MOUSE
	7	17.22	69.8	483 2 Q495M3_HUMAN
	8	17.13	69.4	483 2 Q62WKS5_HUMAN
	9	17.11	69.3	483 2 Q726B5_HUMAN
	10	16.99	68.8	478 2 Q8BBHK3_MOUSE
	11	16.98	68.7	478 2 Q8JZP1_MOUSE
	12	16.98	68.4	479 2 Q6NRA6_XENIA
	13	16.77	67.5	481 2 Q8K415_RAT
	14	15.92	64.5	313 2 Q86YK4_HUMAN
	15	14.76	59.8	470 2 Q726B4_HUMAN
	16	14.76	59.8	470 2 Q6ZRU4_HUMAN
	17	14.50	59.6	470 2 Q495N2_HUMAN
	18	14.50	58.7	477 2 Q4V8B1_RAT
	19	14.47	58.6	511 2 Q495N3_HUMAN
	20	14.16	57.4	477 2 Q811P0_MOUSE
	21	14.15	57.3	477 2 Q8CH37_MOUSE
	22	13.51	54.7	490 2 Q4S4A7_TETNG
	23	13.01	52.7	455 2 Q62M7_HUMAN
	24	12.75	51.7	500 2 Q8C077_MOUSE
	25	12.65	51.3	500 2 Q8CH36_MOUSE
	26	12.55	50.9	504 2 Q6YBV0_HUMAN
	27	12.53	50.7	510 2 Q6DDP2_XENIA
	28	12.53	50.7	522 2 Q4KL91_XENIA
	29	12.44	50.4	504 2 Q86X30_HUMAN
	30	10.80	43.7	285 2 Q495M4_HUMAN
	31	10.60	43.0	301 2 Q5R828_PONPY

RESULT 1 S36A1 HUMAN	STANDARD;	PRT:	476 AA.
ID S36A1 HUMAN			
AC Q7Z2H8; Q7Z7CQ0; Q96M74;			
DT 16-AUG-2004, integrated into UniProtKB/Swiss-Prot.			
DT 01-OCT-2003, sequence version 1.			
DT 07-MAR-2006, entry version 20.			
DE Proton-coupled amino acid transporter 1 (Proton/amino acid transporter 1) (Solute carrier family 36 member 1).			
DE 1) (Solute carrier family 36 member 1).			
GN Name=SLC36A1; Synonyms=AT1;			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;			
OC Homo.			
NCBI_TaxID=9606;			
OX [1] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).			
RN [1] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).			
RP Chen Z, Pei Y-J., Huang W., Anderson C.M.H., Wake K.A.,			
RA Thwaites D.T., Ganpathy V.,			
RA "Structure and function of a proton-coupled amino acid transporter (hPAT1) cloned from the human intestinal cell line Caco2.";			
RT Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.			
RN [2] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND FUNCTION.			
RP [2] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1), AND FUNCTION.			
RC [2] NUCLEOTIDE SEQUENCE [mRNA] (ISOFORM 1).			
RC TISSUE=Intestine; AC AC039481.0; PubMed=12694810;			
RC MEDLINE=12694810; PubMed=10.1016/S0888-7543(03)00099-5;			
RC Boll M., Foltz M., Rubio-Alliga I., Daniel H.,			
RC "A cluster of proton/amino acid transporter genes in the human and mouse genomes.";			
RT Genomics 82:47-56 (2003).			
RL [3] NUCLEOTIDE SEQUENCE [LARGE SCALE RNA] (ISOFORM 1).			
RP [3] NUCLEOTIDE SEQUENCE [LARGE SCALE RNA] (ISOFORM 1).			
RC TISSUE=Endometrial tumor;			
RC The German cDNA consortium;			
RC Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
RL [4] NUCLEOTIDE SEQUENCE [LARGE SCALE RNA] (ISOFORM 2).			
RP [4] NUCLEOTIDE SEQUENCE [LARGE SCALE RNA] (ISOFORM 2).			
RC TISSUE=Testis;			
RC PubMed=14702039; DOI=10.1038/ng1205;			
RC Sudo H., Hosoi T., Karu Y., Kodaira H., Kondo H., Sugiyama T., Irie R.,			
RA Ota T., Suzuki Y., Nishikawa T., Otuki T., Sugiyama T., Irie R.,			
RA Wakamatsu A., Hayashi K., Sato H., Naga I. K., Kimura K., Makita H.,			
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahori K.,			
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA Sudo H., Hosoi T., Karu Y., Kodaira H., Kondo H., Sugiyama T., Irie R.,			
RA Takahashi M., Kanda K., Yoko T., Furuya T., Kikkawa E., Omura Y.,			
RA Abe K., Kamihara K., Sato K., Tanaka T., Kimura K., Makita H.,			
RA Nishimura K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA Tana T., Kimura M., Watanabe M., Hirao S., Chiba Y., Ishida S.,			
RA Ono Y., Takiuchi S., Watanabe S., Yosida M., Horuta T., Kusano J.,			
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,			
RA Yagihara S., Komi F., Hara R., Takeuchi K., Arita M., Inoue N.,			
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			

RA	Moriya S., Momiyama H., Satoch N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Kumagai A., Fukuzumi Y., Kawakami B., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiiwara T., Ono T., Yamada K., Fujii T., Ozaki K., Hirako M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikeda Y., Okamoto S., Oikatani R., Kawakami T., Noguchi S., Iton T., Shigeta K., Senba T., Matsunaga K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Ohya M., Hata H., Watanabe M., Komatsu T., Nakagawa K., Mizushima-Sugano J., Satoch T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Matsuo H., Yamashita R., Okai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs." RT	FT	CONFFLICT	461	AA;	461	Q -> R (in Ref. 4).
CC	-!- FUNCTION: Neutral amino acid/proton symporter. Has a pH-dependent electrogenic transport activity for small amino acids such as glycine, alanine and proline. Besides small apolar L-amino acids, it also recognizes their D-enantiomers and selected amino acid derivatives such as gamma-aminobutyric acid (By similarity). CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Lysosomal and plasma membrane (By similarity). CC -!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2; Name=1; IsoId=Q7Z2HB-1; Sequence=Displayed;	FT	SEQUENCE	476	AA;	530765	MW; 628ae7FC/TA65559F0 CRC64;
CC	Name=2; IsoId=Q7Z2HB-2; Sequence=VSP_011314;	FT	Query Match	100.0%	Score 2469;	DB 1;	Length 476;
CC	Note=No experimental confirmation available;	FT	Best Local Similarity	100.0%	Pred. No. 9	6e-171;	
CC	-!- SIMILARITY: Belongs to the amino acid/polyamine transporter 2 family.	FT	Matches	476	Conservative	0;	Indels 0; Gaps 0;
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a> Distributed under the Creative Commons Attribution-NoDerivs License	FT	RESULT 2				
CC	EMBL: APF16142; APF47194_1; mRNA; EMBL: AY162213; AY011787_1; mRNA; DR: AP057340; BAB71435_1; mRNA; Ensembl: ENSG0000123643; Homo sapiens. HGNC: HGNCA18761; SLC36A1. MIM: 605561; gene. InterPro: IPR02422; AA/rel_permease2. InterPro: IPR013057; AA_transp_TM. DR: P01490; AA_transp_1. KW: Alternative splicing; Amino-acid transport; Glycoprotein; Membrane; Symport; Transmembrane; Transport. CHAIN 1 476 Proton-coupled amino acid transporter 1. /FTid=PRO_0000093835.	FT	Q4RTM7 MACFA		PRELIMINARY;	PRT;	476 AA.
FT	TRANSMEM 52 72 Potential.	FT	Q4RTM7 MACFA		AC	Q4RTM7;	
FT	TRANSMEM 79 99 Potential.	FT	Q4RTM7 MACFA		DT	19-JUL-2005;	integrated into UniProtKB/TremBL.
FT	TRANSMEM 142 162 Potential.	FT	Q4RTM7 MACFA		DT	19-JUL-2005;	sequence version 1.
FT	TRANSMEM 191 211 Potential.	FT	Q4RTM7 MACFA		DT	07-FEB-2006;	entry version 5.
FT	TRANSMEM 216 236 Potential.	FT	Q4RTM7 MACFA		DE	Testis cDNA, clone: Qsa-14788,	similar to human solute carrier family 36 (proton/amino acid symporter), member 1 (SLC36A1).
FT	TRANSMEM 258 278 Potential.	FT	Q4RTM7 MACFA		DE	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	
FT	TRANSMEM 290 310 Potential.	FT	Q4RTM7 MACFA		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Cercopithecidae; Cercopithecinae; Macaca.	
FT	TRANSMEM 343 363 Potential.	FT	Q4RTM7 MACFA		OC	OC	
FT	TRANSMEM 373 393 Potential.	FT	Q4RTM7 MACFA		OC	OC	
FT	TRANSMEM 398 418 Potential.	FT	Q4RTM7 MACFA		OX	NCBI_TaxID=5541;	
FT	TRANSMEM 440 460 Potential.	FT	Q4RTM7 MACFA		OX		
FT	CARBOHYD 31 31 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CARBOHYD 45 45 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CARBOHYD 110 110 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CARBOHYD 174 174 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CARBOHYD 183 183 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CARBOHYD 470 470 N-linked (GlcNAc. . ) (Potential).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	VARSPLIC 359 400 Missing in isoform 2.	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	/FTid=VSP_011314.	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CONFFLICT 72 72 V -> A (in Ref. 4).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CONFFLICT 394 394 P -> L (in Ref. 1).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CONFFLICT 446 446 V -> G (in Ref. 1).	FT	NUCLEOTIDE SEQUENCE.		RN		
FT	CONFFLICT 449 449 VV -> GG (in Ref. 1).	FT	NUCLEOTIDE SEQUENCE.		RN		
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a> Distributed under the Creative Commons Attribution-NoDerivs License	CC	CC				
CC	DR: AB168788; BAB00895.1; -; mRNA.	CC	CC				





DR	InterPro; IPR013057; AA_transpt_TM.
DR	PF01490; AA_transpt; Glycoprotein; Membrane; Symport; Transmembrane;
KW	Amino-acid transporter; Glycoprotein; Membrane; Symport; Transmembrane;
KW	Transport.
FT	CHAIN 1 475
FT	TRANSMEM 51 71
FT	TRANSMEM 78 98
FT	TRANSMEM 141 161
FT	TRANSMEM 190 210
FT	TRANSMEM 215 235
FT	TRANSMEM 257 277
FT	TRANSMEM 289 309
FT	TRANSMEM 342 362
FT	TRANSMEM 372 392
FT	TRANSMEM 397 417
FT	TRANSMEM 439 459
FT	CARBODY 43 43
FT	CARBODY 133 133
FT	CARBODY 173 173
FT	CARBODY 182 182
FT	CARBODY 469 469
FT	CONFLICT 43 43
FT	CONFLICT 198 198
SQ	SEQUENCE 475 AA; 52466 MW;
Query Match	86.7%; Score 2141.5; DB: 2; Length 475;
Best Local Similarity	85.9%; Pred. No. 5.5e-147;
Matches 409; Conservative	33; Mismatches 33; Indels 1; Gaps 1;
Db	1 MSTQRNRNEDTHDSSSTDVSPESPESEGVLNLSSPGSYQRFQGSNSTTWFTLTHLKG 59
Qy	1 MSTQRNRNEDTHDSSSTDVSPESPESEGVLNLSSPGSYQRFQGSNSTTWFTLTHLKG 60
Db	1 MSTQRNRNEDTHDSSSTDVSPESPESEGVLNLSSPGSYQRFQGSNSTTWFTLTHLKG 59
Qy	61 IGTGLIGLPLAVKAGTIVMGPISLTLIGIVAVHCMGLVKAHHFCCRNLKSFVYDGT 120
Db	60 IGTGLIGLPLAVKAGTIVMGPISLTLIGIVAVHCMGLVKAHHFCCRNLKSFVYDGT 119
Qy	121 MYGLESSPCSWLNRNAAHWGRVYDFFLFLVTOLGFCVVYFVLADNFKQVIEAANGTTNC 180
Db	120 MYGLECSPSWLNRNAAHWGRVYDFFLFLVTOLGFCVVYFVLADNFKQVIEAANGTTNC 179
Qy	181 HNNETVLTTPMDSLRMLYMLSPFLPLVFLVFLRNRLALSIFSLNLTMLYSLVMIYQFIV 240
Db	180 NNNVTVTPMDSLRMLYMLSPFLPLVFLVFLRNRLALSIFSLNLTMLYSLVMIYQFIV 239
Qy	241 QRIDPSHLPLVAPWKTYPFLFGTALIFSEFGIMWPLLENRMKDPRKFPLILYGMVIT 300
Db	240 QRIDPSHLPLVAPWKTYPFLFGTALIFSEFGIMWPLLENRMKDOSKFPPLILYGMVIT 299
Qy	301 ILYISLGCLGTLQFGANIQGSITLNLPCNWLQSVKLILYSGIGFFTYALQYVPAIIIP 360
Db	300 VLYISLGCLGTLQFGANIQGSITLNLPCNWLQSVKLILYSGIGFFTYALQYVAAIIIP 359
Qy	361 FFVSRAPHECLVVDLFLRTVFLCILCLAILIPRLDVLISVGSSVSSALALIIPPLE 420
Db	360 AIVSRPHEFLMDLFLRTVFLCILCLAILIPRLDVLISVGSSVSSALALIIPPLE 419
Qy	421 VTFYSEGMSPLTIFKDALISLGFGVYVGTBALYELIOPSNAPIFINSTCAFI 476
Db	420 VTFYSEGMSPLTIFKDALISLGFGVYVGTBALYELIOPSNAPIFINSTCAFI 475
RESULT 6	
Q5F227_MOUSE	PRELIMINARY;
ID	Q5F227_MOUSE
AC	Q5F227_
DT	07-FEB-2005, integrated into UniProtKB/TrEMBL.
DT	10-MAY-2005, sequence version 1.
DT	07-FEB-2006, entry version 4.
DB	Solute carrier family 36 (Proton/ amino acid symporter), member 1.
GN	Name=SLC36A1; ORFNames=RP24-239D8.3-001;
OS	Mus musculus (Mouse).
NCBI_TaxID	9606;
RESULT 7	
Q495M3_HUMAN	PRELIMINARY;
ID	Q495M3_HUMAN
AC	Q495M3_
DT	13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT	13-SEP-2005, sequence version 1.
DT	13-SEP-2005, sequence version 2.
DT	07-FEB-2006, entry version 2.
DE	Solute carrier family 36 (Proton/ amino acid symporter), member 2.
GN	Name=SLC36A2;
OS	Homo sapiens (Human).
NCBI_TaxID	9606;



Db	307	TSLYIGMAALGYLRFGDDIKASISNLNPNCWLYQSVKLLYAGIILCTYALQFYVPAEII	366	Db	307	tsLYIGMAALGYLRFGDDIKASISNLNPNCWLYQSVKLLYAGIILCTYALQFYVPAEII	366
Qy	360	PFEVSRAPHECELYDVFVPTVLYCUTCTTCAILAILIPLDLVIVS19		Qy	360	PFEVSRAPHECELYDVFVPTVLYCUTCTTCAILAILIPLDLVIVS19	
Db	367	PFASISVSTRKWLPLDLISRLMVCILCAILIPRLDLVISMGSVGTALIPLLL	426	Db	367	PFASISVSTRKWLPLDLISRLMVCILCAILIPRLDLVISMGSVGTALIPLLL	426
Qy	420	EVTTTSEGSNPLTFKDALISILGFVGFVGTYBALVELI1QPSNAPIFINST	472	Qy	420	EVTTTSEGSNPLTFKDALISILGFVGFVGTYBALVELI1QPSNAPIFINST	472
Db	427	EVTTTSEGSNPLTFKDALISILGFVGFVGTYQALDELLKSESHPPFSNST	479	Db	427	EVTTTSEGSNPLTFKDALISILGFVGFVGTYQALDELLKSESHPPFSNST	479
<hr/>							
RESULT 9							
Q7Z6B5_HUMAN	Q7Z6B5_HUMAN	PRELIMINARY;	PRT;	483 AA.	Q8BHK3_MOUSE	PRELIMINARY;	PRT;
AC	07Z6B5;				Q8BHK3_MOUSE		
DT	01-OCT-2003	integrated into UniProtKB/TREMBL.			AC		
DT	01-OCT-2003	sequence version 1.			DT	01-MAR-2003	
DT	07-FEB-2006	entry version 14.			DT	01-MAR-2003	sequence version 1.
DE	Proton/amino acid transporter 2.				DT	07-FEB-2006	entry version 24.
GN	Name=SLC6A2; Synonyms=PAT2;				DE	Adult male aort and vein cDNA, RIKEN full-length enriched library (trandorin 1) (Activated spleen cDNA, RIKEN full-length enriched library, clone:AS40067G19 product:similar to LYSOSOMAL AMINO ACID TRANSPORTER 1 (proto/amino acid symporter), member 2, full insert sequence) (Adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330106121 product:similar to LYSOSOMAL AMINO ACID TRANSPORTER 1) (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110065P15 product:solute carrier family 36 (proton/amino acid symporter), member 2, full insert sequence) (Transmembrane domain rich protein).	
OS	Homo sapiens (Human).				DE	DE	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Homo.				GN	Name=SLC6A2; Synonyms=Tramdi; ORFNames=RP24-239D8.1-001;	
OC					OS	Mus musculus (Mouse)	
OC					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.	
OX					OC		
RN	[1]				OX	NCBI_TaxID=10990;	
RP	NUCLEOTIDE SEQUENCE.				RN	[1]	
RC	TISSUE=Testis;				RP	NUCLEOTIDE SEQUENCE.	
RX	PMID=21694810;				RC	STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein, Diencephalon, and Whole body;	
RA	PubMed=12809675;				RX	DOI=10.1126/science.1112014;	
RA	Boll M., Foltz M., Rubio-Alvarez I., Daniel H.;				RA	DOI=16141072; DOI=10.1126/science.1112014;	
RT	"A cluster of proton/amino acid transporter genes in the human and mouse Genomes."				RA	DOI=927953; PubMed=10349636;	
RL	Genomics 82: 47-56 (2003).				RA	DOI=10.1016/S0076-6879(99)03004-9;	
CC	Copyright by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>				RA	DOI=927953; PubMed=10349636;	
CC	Distributed under the Creative Commons Attribution-NoDerivs License				RA	DOI=10.1016/S0076-6879(99)03004-9;	
CC					RA	"High-efficiency full-length cDNA cloning.";	
CC					RA	Methods Enzymol. 303:19-44 (1999).	
DR	IPR013057; AA transport.				RN	[2]	
DR	IPR013057; AA transport.				RP	NUCLEOTIDE SEQUENCE.	
DR	Pfam:PF01490; Aa_trans_1;				RC	STRAIN=C57BL/6J, and NOD; TISSUE=Activated spleen, Aorta and vein, Diencephalon, and Whole body;	
DR	ENSEMBL: ENSG000001863335; Homo sapiens.				RX	DOI=16141072; DOI=10.1126/science.1112014;	
DR	LinkHub; Q7Z6B5; -				RA	DOI=16141072; DOI=10.1126/science.1112014;	
GO	GO:0016020; C:membrane; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO:0006865; P:amino acid transport; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
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DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
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DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;				RA	DOI=927953; PubMed=10349636;	
DR	SEQUENCE	483 AA;	53227 MW;	92B8CE638F56673 CRC64;	RC	DOI=10.1016/S0076-6879(99)03004-9;	
DR	LinkHub; Q7Z6B5; -				RX	DOI=927953; PubMed=10349636;	
DR	GO: GO:0016020; C:membrane; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	GO: GO:0005279; F:amino acid:polyamine transporter activity; IEA.				RA	DOI=927953; PubMed=10349636;	
DR	GO: GO:0006865; P:amino acid transport; IEA.				RA	DOI=10.1016/S0076-6879(99)03004-9;	
DR	InterPro:IPR012422; AA/rel1 permease2.				RA	DOI=927953; PubMed=10349636;	
DR	InterPro:IPR013057; AA transport.				RA	DOI=927953; PubMed=10349636;	
DR	Pfam:PF01490; Aa_trans_1;			</			



Qy	20 SPEESPSEGNNLSSPCTSQRFGQSNSTWQFQTLIHLKCONIGTGLLGLPLAVKNAGYM 79	DR	GO; GO:0016021; C:integral to membrane; RCA.
Db	29 SQDPSANGSESEK-----KTKGIGTQFLQVKGNGTGLLGLPLAVKNAGYM 81	DR	GO; GO:0005886; C:plasma membrane; IDA.
Qy	80 GPLSLIIGLIVAVHNGILVYCAHHICRILANKSFVDYGDPMYGLBSSPWSLWNRHAWG 139	DR	GO; GO:0015187; F:glycine transporter activity; IDA.
Db	82 GPLSLIVMGLIACHCMHILVRCAQFCHRILNKPFNDYGDYTMHGLAFSPNWLQHAWG 141	DR	GO; GO:0015180; F:hydroxyl amino acid transporter activity; IDA.
Qy	140 RRVVDFFLIVTQLGFCCVYFVFLADNFKQYTEAANGTTNNCHNETVILTPTMDSRLYML 199	DR	GO; GO:000865; F:L-alanine transporter activity; IDA.
Db	142 RRVVDFFLIVTQLGFCCVYFVFLADNLQKQEAVNSTTISCHKNETVILTPTMDSRLYML 201	DR	GO; GO:0015808; F:L-alanine transport; IDA.
Qy	200 SFLPFLVLYFTRNLRLSIFSLIANTIMLVSIMYOFIVQRTIDPSHLPVAPWKTYP 259	DR	GO; GO:0015992; F:L-proline transport; IDA.
Db	202 SFLPVGFLYFVRNDRVTLFISLISLISLVSILVTAQYIQTEDASQPLVASWKTYP 261	DR	InterPro; IPR02422; AA:rel_permease2.
Db	202 SFLPVGFLYFVRNDRVTLFISLISLVSILVTAQYIQTEDASQPLVASWKTYP 261	DR	InterPro; IPR013057; AA:transpt_TM.
Db	202 SFLPVGFLYFVRNDRVTLFISLISLVSILVTAQYIQTEDASQPLVASWKTYP 261	DR	Pfam; PF0490; AA: transp_1.
Qy	260 LFFGTAISFSPGIGVNLPLLENKMDPKFLILYIGMVIVTILYISLGCLGYLQFGANIQ 319	DR	SEQUENCE 478 AA; 52019 MW; 2E022C59577E8236 CRC64;
Db	262 LFFGTAISFSPGIGVNLPLLENKMDARGFPFTISLGMISLTLYIAIGALGYLRGGDIK 321	DR	Query Match 68.7%; Score 1695.5; DB 2; Length 478;
Qy	320 GSITNLNPNCWLYQSVKLQLYSIGIFTYALQFYVPAEILIPFVRAPEHCELVDFYR 379	DR	Best Local Similarity 72.6%; Pred. No. 1.1e-114; Mismatches 49; Gaps 1;
Db	322 ASITNLNPNCWLYQSVKLQLYSIGIFTYALQFYVPAEILIPFVRAPEHCELVDFYR 381	DR	Matches 329; Conservative 49; Mismatches 68; Gaps 7;
Qy	380 TVLCLTCAILAIPLDLYISLGCVSSSALLIPIPPLLETTYSEGMSPLTIFKDAL 439	DR	20 SPEPSEGNNLSSPCTSQRFGQNSTWQFQTLIHLKCONIGTGLLGLPLAVKNAGYM 79
Db	382 LALVCLTCAILAIPLDLYISLGCVSSSALLIPIPPLLETTYSEGMSPLTIFKDAL 441	DR	29 SQDPSANGSESEK-----KTKGIGTQFLQVKGNGTGLLGLPLAVKNAGYM 81
Qy	440 ISILGVFGFVFGTYEALYELIOPSNAPIFINST 472	DR	Qy 80 GPIISLIIIGIVAVHNGILVYCAHHICRILANKSFVDYGDPMYGLBSSPWSLWNRHAWG 139
Db	442 ISILGFMGFGFVFGTYQALDELIKSGNSPALSNST 474	DR	82 GPLSLIVMGLIACHCMHILVRCAQFCHRILNKPFNDYGDYTMHGLAFSPNWLQHAWG 141
Qy	RESULT 11	DR	140 RRVVFDFLIVTQLGFCCVYFVFLADNFKQYTEAANGTTNNCHNETVILTPTMDSRLYML 199
ID	Q8JZP1_MOUSE	Db	142 RRVVFDFLIVTQLGFCCVYFVFLADNLQKQEAVNSTTISCHKNETVILTPTMDSRLYML 201
AC	Q8JZP1;	Qy	200 SFLPFLVLYFTRNLRLSIFSLIANTIMLVSILVTAQYIQTEDASQPLVASWKTYP 259
DT	01-OCT-2002, integrated into UniProtKB/TREMBL.	Db	202 SFLPFLVLYFTRNLRLSIFSLIANTIMLVSILVTAQYIQTEDASQPLVASWKTYP 261
DT	01-OCT-2002, sequence version 1.	Qy	260 LFFGTAISFSPGIGVNLPLLENKMDPKFLILYISLGCLGYLQFGANIQ 319
DT	07-FEB-2006, entry version 16	Db	262 LFFGTAISFSPGIGVNLPLLENKMDARGFPFTISLGMISLTLYIAIGALGYLRGGDIK 321
DE	Transdor 1 (Proton/amino acid transporter 2).	Qy	320 GSITNLNPNCWLYQSVKLQLYSIGIFTYALQFYVDAEIIIPFFNSRAPEHCELVDFYR 379
GN	Name=Slc36a2; Synonyms=PAT2, Tramdi;	Db	322 ASITNLNPNCWLYQSVKLQLYSIGIFTYALQFYVDAEIIIPFFNSRAPEHCELVDFYR 381
OS	"Mus musculus" (Mouse)	Qy	380 TVLCLTCAILAIPLDLYISLGCVSSSALLIPIPPLLETTYSEGMSPLTIFKDAL 439
OC	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;	Db	382 LALVCLTCAILAIPLDLYISLGCVSSSALLIPIPPLLETTYSEGMSPLTIFKDAL 441
OC	Metazoa; Eutheria; Euchondrocytes; Glires; Rodentia; Sciurognathii;	Qy	440 ISILGFVFGTYEALYELIOPSNAPIFINST 472
OC	Muroidea; Muridae; Murinae; Mus.	Db	442 ISILGFVFGTYEALYELIOPSNAPIFINST 474
RN	[1]	NUCLEOTIDE SEQUENCE	RESULT 12
RP	STRAIN=CS/BL/6; TISSUE=Pou3f1 mutant sciatic nerves;	Q6NR26_XENLA	Q6NR26_XENLA PRELIMINARY; PRT: 479 AA.
RX	MEDLINE=22338849; PubMed=12451123;	ID	Q6NR26_XENLA PRELIMINARY; PRT: 479 AA.
RA	Berningham J.R. Jr., Shumas S., Whisenhant T., Sirkowski E.E.,	AC	Q6NR26;
RA	O'Connell S., Scherer S.S., Rosenfeld M.G., Daniel H.,	DT	05-JUL-2004, integrated into UniProtKB/TrEMBL.
RT	"Identification of genes that are downregulated in the absence of the POU domain transcription factor pou3f1 (Oct-6, Tst-1, SCIP) in sciatic nerve."	DT	05-JUL-2004, sequence version 1.
RT	J. Neurosci. 22:10217-10231 (2002).	DT	07-PEB-2006, entry version 13.
RN	[2]	RA	MGCB4608_protein.
RP	NUCLEOTIDE SEQUENCE.	GN	Xenopus laevis (African clawed frog).
RC	STRAIN=CS/BL/6;	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RX	MEDLINE=22063354; PubMed=11959859; DOI=10.1074/jbc.M200374200;	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Bipoidea; Pipidae;
RA	Boll M., Foltz M., Rubio-Alvarez I., Kottra G., Daniel H.,	OC	Xenopoda; Xenopus; Xenopus.
RA	"Functional characterization of two novel mammalian electrogenic proton-dependent amino acid cotransporters.";	NCBI_TaxID=8335;	XNCBI_TaxID=8335;
RT	J. Biol. Chem. 27:2966-2973 (2002).	RN	[1]
CC	Copyright by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>	RP	NUCLEOTIDE SEQUENCE.
CC	Distributed under the Creative Commons Attribution-NoDerivs License	RC	TISSUE=Oocytes;
CC	DR EMBL; AF512429; AFAM4854.1; mRNA.	RX	MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;
DR	Ensembl; AF51244; AFAM0481.1; mRNA.	RA	DR Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
DR	Ensembl; ENSMUSG0000020264; Mus musculus.		
DR	MGII; MGII:1891430; SIC36a2.		





Best Local Similarity	62.2%	Pred.	No. 9.5-e-99;	Indels	5;	Gaps	5;
Matches	291;	Conservative	77;	Mismatches	95;		
Qy	6	LRNEDWH-DYSSSTDVSPPEESPESEGNNLNSPSPSYQRQGSNSTTWFQTLIHLKGKNGTG	64				
Db	3	LIGRLRSENLSDNG-QSPLPSSSSSTTSENVHPA-GEA-GLSMMQTLIHLKGKNGTG	59				
Qy	65	LLGLPLPAVKHAGIVMGPISLILIGIVAHCMGTLVKGCAAHFCCRNLNSFVDYGDTCYMYGL	124				
Db	60	LLGLPLPAKINGLLGVGPKSLAIGVLTWCHMVLINCAQHLSQRQKIFVNGEATMGL	119				
Qy	125	ESSPCWLRNHAHMGRAVDFELIVTOLGECCYFVFLADNEKQVIEAANGTNNCHNNE	184				
Db	120	ETCPNTWLRATAVWGRYTVSFLLVITQLGFCSCVYFPMWADNLQMQMVERAHTSNCQPRE	179				
Qy	185	TVLTLPTMDSERLYMLSFPLFLVLYFIRNLRAISIIFSLANITMLVSLVMIYOFIVQRSP	244				
Db	180	ITLTFLIDTIFYMLFLIPFLMLVQNLKLSVFTLANTITLGMALIPIYMECIP	239				
Qy	245	DPSHLPLVAPKRTYPLFFGTAFLSPSEGIGMVLPLBKMDPKFKPLLYLGKMYVITLYI	304				
Db	240	YPSNLPLMANWPKTLFFGTAIFTFCYGMVLPLKQNMKHPQOFSFYLGMGSIVITLYI	299				
Qy	305	SLGLGQLQGANIQSSITLNIPNCWLIQSVLILYI	364				
Db	300	LLGTGQMKFESSDTQASITLNIPNCWLIQSVKLIMYSIGIFFYALQFVPAETIIPPAIS	359				
Qy	365	RAPEHCELVWDLFVRYTFLCUTCILALIIPRLDVLSVGSYSSALIIPPLLEYTTF	424				
Db	360	QVSESSWALFVDSLVSRAVCLCUTCISALIIPRLDVLSVGSYSSALIIPALLETVIF	419				
Qy	425	YSEGMSPLTIFKDALLISLGFMGVFGVWGTYTALEYLIPSNAPFINST	472				
Db	420	YSEPMSCMTTAKDITMSIYVGLIGCTYQAYFELPQPTSHM-ANST	466				

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GenCore version 5.1.9

OM protein - protein search, using sw mode:1

Run on: August 24, 2006, 01:25:09 ; Search time 50 Seconds (without alignments)

833.292 Million cell updates/sec

Title: US-10-679-362-2

Perfect score: 2469

Sequence: 1 MSTQRLRNEDHYSSSTDVS.....YELIQPSNAPIFINSTCAFI 476

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5\_COMB.pep:\*

2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6\_COMB.pep:\*

3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7\_COMB.pep:\*

4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H\_COMB.pep:\*

5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/PETUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

## ALIGNMENTS

RESULT 1  
US-10-094-749-3076 ; Sequence 3076, Application US/10094749

; Patent No. ~6979557

## GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO  
APPLICANT: SUGIYAMA, TOMOYASU  
APPLICANT: OTSUKI, TETSUJI  
APPLICANT: WAKAMATSU, AI  
APPLICANT: SATO, HIROYUKI  
APPLICANT: ISHII, SHIZUKO  
APPLICANT: YAMAMOTO, JUN-ICHI  
APPLICANT: ISONO, YUKO  
APPLICANT: HIO, YURI  
APPLICANT: OTSUKA, KAORU  
APPLICANT: NAGAI, KEIICHI  
APPLICANT: IRIE, RYOTARO  
APPLICANT: TAMECHIKA, ICHIRO  
APPLICANT: SEKI, NAOKI  
APPLICANT: YOSHIKAWA, TSUTOMU  
APPLICANT: OTSUKA, MOTOKI  
APPLICANT: NAGAHARI, KENJI  
APPLICANT: MASHIO, YASUHIKO

TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA  
FILE REFERENCE: 084335/0160  
CURRENT APPLICATION NUMBER: US/10/094,749  
CURRENT FILING DATE: 2002-03-12  
PRIOR APPLICATION NUMBER: 60/350,435  
PRIOR FILING DATE: 2002-01-24  
PRIOR APPLICATION NUMBER: JP 2001-328381  
PRIOR FILING DATE: 2001-09-14  
NUMBER OF SEQ ID NOS: 3381  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 3076  
LENGTH: 434  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-094-749-3076  
Query Match 89.8%; Score 2217; DB 2; Length 434;

Best Local Similarity 90.8%; Pred. No. 2.4e-221;  
Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;

Qy 1 MSTQRLRNEDHYSSSTDVSPEPSEGGLANNLSSPGSYQRFQGSNSTWFTQLHLKGN 60  
Db 1 MSTQRLRNEDHYSSSTDVSPEPSEGGLANNLSSPGSYQRFQGSNSTWFTQLHLKGN 60  
Qy 61 IGTGLGLPLAVKAGITVMGPISLILLIGIVAVHCMGILVKAHHCPRLINKSFVYCDTV 120

27 169 6.8 136 2 US-09-270-767-31761  
28 169 6.8 136 2 US-09-270-767-46978  
29 169 6.8 447 2 US-09-370-253-2  
30 166.5 6.7 504 2 US-09-640-19C-77  
31 165 6.7 505 2 US-09-919-497-07  
32 165 6.7 505 2 US-09-949-016-11556  
33 164 6.6 134 2 US-09-270-767-42974  
34 162.5 6.6 134 2 US-09-270-767-42974  
35 160.5 6.5 511 2 US-09-248-796A-20816  
36 157.5 6.4 90 2 US-09-178-093B-87  
37 140.5 5.7 154 2 US-09-270-767-31638  
38 140.5 5.7 154 2 US-09-270-767-46855  
39 139.5 5.6 90 2 US-09-178-093B-40  
40 138.5 5.6 90 2 US-09-602-787A-530  
41 136 5.5 415 2 US-09-602-787A-530  
42 133 5.4 116 2 US-09-270-767-32714  
43 133 5.4 116 2 US-09-270-767-7931  
44 127 5.1 259 2 US-09-370-253-4  
45 122.5 5.0 463 2 US-09-583-110-5223

27 169 6.8 136 2 US-09-270-767-31761  
28 169 6.8 136 2 US-09-270-767-46978  
29 169 6.8 447 2 US-09-370-253-2  
30 166.5 6.7 504 2 US-09-640-19C-77  
31 165 6.7 505 2 US-09-919-497-07  
32 165 6.7 505 2 US-09-949-016-11556  
33 164 6.6 134 2 US-09-270-767-42974  
34 162.5 6.6 134 2 US-09-270-767-42974  
35 160.5 6.5 511 2 US-09-248-796A-20816  
36 157.5 6.4 90 2 US-09-178-093B-87  
37 140.5 5.7 154 2 US-09-270-767-31638  
38 140.5 5.7 154 2 US-09-270-767-46855  
39 139.5 5.6 90 2 US-09-178-093B-40  
40 138.5 5.6 90 2 US-09-602-787A-530  
41 136 5.5 415 2 US-09-602-787A-530  
42 133 5.4 116 2 US-09-270-767-32714  
43 133 5.4 116 2 US-09-270-767-7931  
44 127 5.1 259 2 US-09-370-253-4  
45 122.5 5.0 463 2 US-09-583-110-5223







RESULT 8  
 US-09-854-774-2  
 Sequence No. 6809233  
 GENERAL INFORMATION:  
 APPLICANT: FROMMER, Wolf-Bernd  
 TITLE OF INVENTION: DNA SEQUENCES FOR AN AMINO ACID  
 TRANSPORTER, PLASMIDS, BACTERIA, YEASTS AND PLANTS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Ostrolenk, Faber, Gerb & Soffen  
 STREET: 1180 Avenue of the Americas  
 CITY: New York  
 COUNTRY: US  
 STATE: NY  
 ZIP: 10036-8403  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/854,774  
 FILING DATE: 14-May-2001  
 CLASSIFICATION: <Unknown>  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/964,939  
 FILING DATE: 1998-05-28  
 APPLICATION NUMBER: US 08/007,636  
 FILING DATE: 21-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meilman, Edward A.  
 REGISTRATION NUMBER: 24,735  
 REFERENCE/DOCKET NUMBER: P/951-107  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 382-0700  
 TELEFAX: (212) 382-0888  
 TELEX: 236925  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:

LENGTH: 485 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-854-774-2

Query Match 8.7%  
 Best Local Similarity 20.0%; Pred. No. 1.7e-13; Length 485;  
 Matches 101; Conservative 81; Mismatches 221; Indels 103; Gaps 15;

Qy 8 NEDDYDYSSTDVSPBSPSPEGLANNSPGSYQRFSQNSNTWQFLILHKGNIQTGILG 67  
 S NTEGHINHSTAESGDDAYTSDPTKNTDEDGREKRTG----TWLTASAHTTAVIGSGVLS 59

Db 68 LPLAVTKNAGIVMGPSSLLTIGIVATHCMGILVKC--AHFRCRINKSFDYGDPTVMYGL 124  
 60 LAWAAQOLGVIAGTSLILLFSFITYFTSTMILADCFTRDPVTGKNTYMDVVRSLGGR 119

Qy 125 ESSPCSWLRLNHAHNRRVVDFFELVITQLGFCVVYFVFLADNEFKQVIEANGTTNNCHNNE 184  
 Db 120 KVQLC---GVAQGN----LIGTVGTTITASISLYAVGK-----SNCFHDK 159

Qy 185 TVLTPMTSRLYMSFLPFLVLLFIRNLRLSFLSLLANI-----226  
 Db 160 GHTACTISNYPYMAVFGIQLQVILSQIPNFKLSSLIVMAVMSPTYATIGIGLIAITVA 219

Qy 227 -----TMVLVSLVNTYQFIVTQFLPFLVLLFIRNLRLSFLSLLANI-----FGTAIFSEG 271  
 Db 220 GGKVGTTSMTGTAQVGDVTAQK-----WRSFAVGDAFAYAYATVILBIQD 268

Qy 272 IGMVPLLENKMDPKFPPLILYLGIVLQFGGANIQSITLN--LPN 328  
 Db 269 TLRSSPAENQAM--KRAISLV--GVSTTTFYILCGCIGTAAGNNAPGDFLTDFGFFEP 323

Qy 329 CWLYQ-----SVKLKLYSGLIFTYALQF-----YVPAEIIIPFFVSRAPEECELVV 374  
 Db 324 FWLIDFANACTAVHLIGAYQVFAQPFQFVEKKCMNRNPDPNKFITSEYNSNVPFLGKENI 383  
 Qy 375 DLF---VRTVLYCLTCLALIIPRLDVLVISLGSYSSALALIIPPLBEVTTFSEGMSP 431  
 Db 384 SLFRLVWRTAXVITVAMIPPFNAILGLIGAASFWPLTVYFVEMHIAQTKIKYSA 443

Qy 432 LTI-----FKDALISLGFVGFVYQ 451  
 Db 444 RWIAKTMCTVCLVLSSLLAAGSIAG 469

RESULT 9  
 US-09-599-360B-109  
 Sequence 109, Application US/09/9360B  
 Patent No. 6548633  
 GENERAL INFORMATION:  
 APPLICANT: Dumas Milne Edwards, J.B.  
 APPLICANT: Bouquelaret, L.  
 APPLICANT: Jobert, S.  
 TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
 FILE REFERENCE: GENSET.05CP3  
 CURRENT APPLICATION NUMBER: US/09/599,360B  
 PRIORITY NUMBER: 60/113,686  
 PRIORITY FILING DATE: 1998-12-22  
 PRIORITY APPLICATION NUMBER: 60/141,032  
 PRIORITY FILING DATE: 1999-06-25  
 PRIORITY APPLICATION NUMBER: 60/141,032  
 PRIORITY FILING DATE: 1999-12-21  
 NUMBER OF SEQ ID NOS: 123  
 SOFTWARE: Patent-ppm  
 SEQ ID NO: 109  
 LENGTH: 108  
 TYPE: PRT  
 ORGANISM: Homo Sapiens  
 FEATURE:

NAME/KEY : SIGNAL  
 LOCATION : -28..-1  
 US-09-593-360B-109

Query Match 8.2%; Score 203.5; DB 2; Length 108;  
 Best Local Similarity 48.4%; Pred. No. 3.4e-13; Gaps 2;  
 Matches 45; Conservative 16; Mismatches 23; Indels 9; Gaps 2;

Qy 390 AILPRLDIVTSVGSVSSALALIPLLVEVTFYSEMSPLTFKDALISTLGFVGVFV 449  
 Db 10 AILPRLDIVTSVGSVSSALALIPLLVEVTFYSEMSPLTFKDALISTLGFVGVFV 69

Qy 450 VGTYEALYELIOPS-----NAPIF-INSTC 473  
 Db 70 LGTYTVEEIIYPTSKVVAQTPQSBLFLNINSTC 102

---

RESULT 10  
 US-09-248-796A-20813  
 ; Sequence 20813, Application US/09248796A

; Patient No. 6747137  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keith Weinstock et al  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 ; FILE REFERENCE: 107196.132  
 ; CURRENT APPLICATION NUMBER: US/09/248,796A  
 ; CURRENT FILING DATE: 1999-02-12  
 ; PRIOR APPLICATION NUMBER: US 60/074,725  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 60/096,409  
 ; PRIOR FILING DATE: 1998-08-13  
 ; NUMBER OF SEQ ID NOS: 28208  
 ; SEQ ID NO: 20813  
 ; LENGTH: 399  
 ; TYPE: PRT  
 ; ORGANISM: Candida albicans  
 US-09-248-796A-20813

Query Match 8.2%; Score 202.5; DB 2; Length 483;  
 Best Local Similarity 21.3%; Pred. No. 3.7e-12; Gaps 20;  
 Matches 108; Conservative 76; Mismatches 179; Indels 145; Gaps 20;

Qy 13 DYSSTDVSPEEPSEGIANLSSPGSYQRFQGS---NSTWFTOLIHLJKGNTGTLGHF 69  
 Db 51 DWNSNSVDE--TSEELPLTSRV--STKEHSFSLITGNSTAQTIFNSINTLIGMLSP 107

Qy 70 LAVKNAIGTVMGPISLLIGIVAVHCMGLLVKCAHHFCRRLNSFVVDYDPTVMGLESSPC 129  
 Db 108 LGPKMMSGMFGSLLVVAFLINTTAKYLGKLYR---HQELMTYGDIA----- 153

Qy 130 SWLRNHAHWGR--RVVDFFLITVQLGRCCVYVFVADNF-----KQVTEANGT 176  
 Db 154 -----YAGGKYFLYLVTLFPVDFLFGASLTLLFADFSFTIWPVHPVPAKAIIVAV-- 205

Qy 177 TNANCHNETVLTPTMDSRMLYSFLPFLVFLVFLRNRLSFLSLLANITM-LVSLVM 234  
 Db 206 -----VFLVSLLP-----LSMLSTFSLLGISTVGILSVP 236

Qy 235 YQPIVQRIPDPHSLP-----LVAWPWKTYPFLFFGTAIFSEFGIMV 275  
 Db 237 ICGFLVDTSPGSLLIPATTLLPPNPINLFLSGLIWFAPWGGHPVF----- 282

Qy 276 LPLENKMDPKPEPLILYIGMVIVTLYTISLGCGUFLGQANTQGSTINL-----PN---- 328

Db 283 PELYRDMRHPFKETKSSNISFLTYLDESIGATGYLMGLMDDIVKSIMQNPYPP1 342

Qy 329 -----CWLQSVKL---LYSIGFIFTYALQFVPAELIIPFFYVSRAPEHCELV-----V 374  
 Db 343 INSTLCLINGILPISKLPLVTKITSENIFGIAKTV-----KLDENGKLTDTYGP 396

Qy 375 DLFLVPTVLYCILTCILAILIPRLDVISLVGSVSSALLIIPPLLEVTFY---SEG 428  
 Db 397 RVFSTSFCCVLLISALLTSFCKVAFRLSALCDTVCLTLPL-----FYLKLNRSSVG 451

Qy 174 NGTINCHNETVLTPTMDSRMLYSFL---PFLVLVFLRNRLSFLSLLANITM 229  
 Db 118 -----VTVVPYDBKHTPLFWLAVSTVLTIPPSFLKUDLSKYSSTLGLVAF 165

Qy 166 YMTLIVGIVYFAGDIERQGQTLF-PTSTVGFESTFSIVTFAFTGHONFSIINEAROIS 224  
 Db 230 -VSLMIXYQIVQRIPDPHSLPLYAPWKYPLF---FGTAIFSEFGIMV/PLENKMDFR 286

Qy 287 KFPL--ILYGMVIVTLYISLGCGUFLGQANTQGSTINLPCNWLXSVKLLYSIGF 344  
 Db 225 LTSLTKLNVNPAIGSSLFLAVGLSGYLFGQDVGNVLYPN-----GLTTTGRF 277

Qy 345 -----FTYALQFVPAEL----- 357  
 Db 278 CIVFMVTFSPFLMII-PAIRSINNYYHWTWTNNYFDKDEANESTALLGNESQESQIAEDEB 336

Qy 358 -----IIPFFVSRAPHECCEVYDLYFRTVLYCILTCILAILIPRLDVISVGS 405  
 Db 337 QGKTHLSHVYVPP-----PHKHFV-----VTTSLIIGYLLAISIKSFAFLATVGA 383

CURRENT FILING DATE: 1999-08-09  
 EARLIER APPLICATION NUMBER: 60/097,222  
 EARLIER FILING DATE: August 20, 1998  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO: 10  
 LENGTH: 447  
 TYPE: PRT  
 ORGANISM: *Triticum aestivum*  
 US-09-370-253-10

Query Match 8.0%; Score 197; DB 2; Length 447;  
 Best Local Similarity 21.3%; Pred. No. 1.2e-11; Mismatches 84; Indels 46; Gaps 15;  
 Matches 93; Conservative 84; Gaps 15;

Qy 44 SNSSTWFOQTJHLIKGNITGCGTLLGIPPLAYVNAGIYNGPISLILGIVAVHCMGLIYVKCAH 103  
 Db 33 SRNAKWWYSAFHNTAMVAGCAGVSLYAMSBLGWPGLGIAVLIVSIVVLTILWQVNE-MH 91

Qy 104 HFCRRLINKSFVDYDGTVMGLESSPCWSLVRNHAHNGRRVVDFFLIVTQLGFCCVYFVFLA 163  
 Db 92 EMVP--GKRFDRYHEHGQAFGDKLGLWL-----VVPQQLIV-EVGVNITYMVTGG 139

Qy 164 DNFKVQTEAANGTTCNNHNETVILPTMDRSRLMSLFLVFLVFLVFLVFLVFLVFL 223  
 Db 140 RSLKKFHDFVI - CDGKCKD1KLTFIMAVSHVFLSQLP-----NLNSISGVSLA 188

Qy 224 ANITMLVSLVMIYQFIVQR---IIPDPHSLPLVAPWKTLPF--FGTAFAPSFEIGMVP 277  
 Db 189 AAVMSLSSYLTIAWGAVIDKGRMVDYDNRATTPKVKVGFAGLAEVAYAGHNVLE 248

Qy 278 LE---NKMDPDKPKPLI--LYLGIVVITLILYISLGCLGYLQFGANIQGS--ITLNLPNC 329  
 Db 249 IQATIPTSPERPSKCEPMWKGVVAIVVAVLACYFPVAlIGWAFGNISVDDNLTINKP- 307

Qy 330 WLYQSVKL--LYSIGIFITYALQFYVPAELIIPPFVSRAPHECFLVVDLFLVFLVCLT 386  
 Db 308 WLISTANMMVVIHVIGSYQIYAMPYDFMIETVL--VKUKLKFPPOLTLIARTLYVAFI 364

Qy 387 CILALIPIRDLVLSVGSYSSSALALIIPPLLETTFVSEGMSPLTIFDALSILGPV 446  
 Db 365 MFAVATPFFGFLGFGFFGKPAFAPTYFLPCIMMIAKDRKRS-LSWFTNWVCIVLGYC 423

Qy 447 GFVVGTYEALYELIQS 463  
 Db 424 LMILSPIGGLRQIILDS 440

RESULT 13  
 US-09-270-767-43308  
 Sequence 43308, Application US/09270767  
 Patent No. 6703491  
 GENERAL INFORMATION:  
 APPLICANT: Homburger et al.  
 TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 FILE REFERENCE: File Reference: 7326-094  
 CURRENT APPLICATION NUMBER: US-09-270,767  
 CURRENT FILING DATE: 1999-03-17  
 NUMBER OF SEQ ID NOS: 62517  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO: 43308  
 LENGTH: 150  
 TYPE: PRT  
 ORGANISM: *Drosophila melanogaster*  
 OTHER INFORMATION: xaa means any amino acid  
 US-09-270-767-43308

Query Match 7.9%; Score 196; DB 2; Length 150;  
 Best Local Similarity 35.5%; Pred. No. 3.2e-12; Mismatches 24; Indels 4; Gaps 3;

Qy 22 YPTTLELTPTKSANGSNDDYDPHOREL-KNPNTNFQTFAHFTLKASVGTGVLA 79  
 Db 73 KNAGIVGMGPISLILGIVAVHCMGLIYVKCAHFCRRLNSFVDYDGTVMYGLESSPCCSWL 132  
 Db 80 AHAGYVNGTLLTLLTLLGSLALYCLHLIKCMYILCRLKRQVRYVPSXSQAMNLGLKQGP-PWL 138

Qy 133 R 133  
 Db 139 R 139

RESULT 14  
 US-09-370-253-6  
 Sequence 6, Application US/09370253  
 Patent No. 6165732  
 GENERAL INFORMATION:  
 APPLICANT: Alien, Stephen M.  
 APPLICANT: Tkhorpe, Catherine J.  
 TITLE OF INVENTION: Amino Acid Transporters  
 FILE REFERENCE: BB-1200  
 CURRENT APPLICATION NUMBER: US/09/370,253  
 CURRENT FILING DATE: 1999-08-09  
 EARLIER APPLICATION NUMBER: 60/097,222  
 EARLIER FILING DATE: August 20, 1998  
 NUMBER OF SEQ ID NOS: 18  
 SOFTWARE: Microsoft Office 97  
 SEQ ID NO 6  
 LENGTH: 447  
 TYPE: PRT  
 ORGANISM: *Oryza sativa*  
 US-09-370-253-6

Query Match 7.6%; Score 187.5; DB 2; Length 447;  
 Best Local Similarity 21.7%; Pred. No. 1.2e-10; Mismatches 85; Indels 51; Gaps 18;  
 Matches 95; Conservative 85; Mismatches 206; Indels 51; Gaps 18;

Qy 44 SNSSTWFOQTJHLIKGNITGCGTLLGIPPLAYVNAGIYNGPISLILGIVAVHCMGLIYVKCAH 103  
 Db 32 SRNAKWWYSAFHNTAMVAGVSLSPYANSELGMGPGLGIAVLISWPTILYTLWQVNE-MH 90

Qy 104 HFCRRLINKSFVDYDGTVMYGLESSPCWSLVRNHAHNGRRVYDFFLVTOLGFCCCYFVFLA 163  
 Db 91 EMVP--GKRFDRYHEHGQAHFGEKGKGLWI-----VPPQQLIV-EVGVNIVMVTGG 138

Qy 164 DNFKQ--VIEAANGTTCNNHNETVILPTMDSSLYMLSFLLPFLVLLYFIRNLRLSIF 220  
 Db 139 KSLKXPFHDVILCEGRG---CKNKLITYFIMIFASHTHFLVLSQLP-----NFSISGV 185

Qy 221 SLLANITMLVSLVMMYQFIVQ--RIPDPS-HL-PLVAPWKTPYPLB-FGTAIFSSBEGIM 274  
 Db 186 SLAAVMSLSSYLTIAWGAVIDKGRMVDYDNRATTPKVKVGFAGLAEVAYAGHNV 245

Qy 275 VLPLE---NKMKDPRKEPLI--LYLGIVVITLILYISLGCLGYLQFGANIQGS-ITLNL 326  
 Db 246 VLEIQTIPSEPEKSKKPKWKGVYVAYIIVALCYFPVAlGWFAGNHDDNLTLSR 305

Qy 327 PNCWLY--QSVKLISIGIFTYALQFYVPAELIIPPFVSRAPHECFLVVDLFLVRTVLY 383  
 Db 306 PK-WLIALANMMVVIHVIGSYQIYAMPVDFMIETVL--VKKLRFPPGLTLRLIARTLYV 361

Qy 384 CLTCIILAILPRLDVLVLSVGSVSSSALALIIPPLLETTFVSEGMSPLTIFKDALISIL 443  
 Db 362 AFTMMFAITPFFGGFLGFFGPAFAPTYFLPCIMMIAKDRKRS-LSWFTNWICIL 420

Qy 444 GFVGFGVGTYEALYELI 460  
 Db 421 GVMLNLSPIGGLRQI 437

RESULT 15  
 US-09-640-419C-24

1.4 YSST-DVSEPPSPSEGICINNLSSPGSYQRFQSNSTTWFQTLIHLKGNITGCLPLAV 72

Qy

; Sequence 24, Application US/09640419C  
 ; Patent No. 663015  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bidney, Dennis L.  
 ; APPLICANT: Crasta, Oswald R.  
 ; APPLICANT: Hu, Guihua  
 ; APPLICANT: Lu, Guihua  
 ; TITLE OF INVENTION: DEFENSE-RELATED SIGNALING GENES AND METHODS OF USE  
 ; FILE REFERENCE: 35718/199009 (5718-92)  
 ; CURRENT APPLICATION NUMBER: US/09/640,419C  
 ; CURRENT FILING DATE: 2000-08-17  
 ; PRIOR FILING DATE: 1999-08-18  
 ; PRIOR APPLICATION NUMBER: 60/149, 656  
 ; PRIOR FILING DATE: 1999-08-18  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 24  
 ; LENGTH: 449  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-640-419C-24

Query Match 7.6%; Score 187; DB 2; Length 449;  
 Best Local Similarity 20.7%; Pred. No. 1.4e-10;  
 Matches 82; Conservative 79; Mismatches 188; Indels 48; Gaps 15;

Qy	44	SNSTTWFQTLIHLKGNICTGGLGGLPLAVKAGIVMGPGPLSLIIGIVAWHCMGILVYCAH	103
Db	28	SRNAKMWYSAFHNTAMVAGVLSPYANSNLGPGVTTIMMSWITLYLQMVB-MH	86
Qy	104	HFC--RRLNKSFDVGDITYMGLSSPCWLNRHAHGRVYDFELIVTQLGRCCVYTF	161
Db	87	EIVPGKRLR---YHELGQHAFGEKLGLWI-----VVPQQLIVEVGDIVVMT	132
Qy	162	LADNPKQVTEAANGTTNNCHNNETVILPTMDSSLMLFLPPFLVLYTFRNLRLSIFS	221
Db	133	GGASLKKVHQL--VCPDCEKIRTFWIMIFASFYHVFISHLP-----NNSNISLIS	180
Qy	222	LLANITMVLSLVMYQFIYOR--LPDPSPHLPLVAP--WPTYPLF--FGTAIFSEFGICMV	275
Db	181	LAAAVMSLTYSTIWAASVHKGVHPDVDSPRASTDVGKVNFINALGVAFAYAGHNNV	240
Qy	276	LPLENKMKD---PRKFPLI-LYLGMYVYTLXISLGCLGYLQFGANIQGSITLNJPN-	328
Db	241	LEIQATIPSPPEMPSKVMWRGVIVAYIVIAICYFPVAFLGYYTFGNSVDDNLITLBRP	300
Qy	329	CWLYOSVKLILYSIGIFFFFVLAQFVY----PA-BLI1PFVSRAPEHCELVVDLFVRFVL	382
Db	301	IWLAMANMFVWVHIGSQVFFHLIFAMPVFDMLETVLVKKMNENPSFLRFTTSLY	360
Qy	383	VCLTCILATLIPRLDVLISVGSVSSAALALIIPLL 419	
Db	361	VAFTMVAICVPFFGGLQGFGGFAFAPPVYLDICIM 397	

Search completed: August 24, 2006, 01:26:34  
 Job time : 51 secs

Result	No.	Score	Query	Match	Length	DB	ID	Description
- 1	2469	100.0	476	3	US-09-805-456-2			Sequence 2, Appli
- 2	2469	100.0	476	4	US-10-225-810-21			Sequence 21, Appli
- 3	2469	100.0	476	4	US-10-679-362-2			Sequence 2, Appli
- 4	2460	99.6	496	4	US-10-080-334-22			Sequence 22, Appli
- 5	2402.5	97.3	568	4	US-10-332-447-8			Sequence 8, Appli
- 6	2398	97.1	500	4	US-10-080-334-20			Sequence 20, Appli
- 7	2324	94.1	476	3	US-09-805-456-7			Sequence 7, Appli
- 8	2217	89.8	434	4	US-10-694-749-3076			Sequence 3076, Ap
- 9	2217	89.8	434	4	US-10-080-334-137			Sequence 137, Ap
- 10	2217	89.8	434	4	US-10-080-334-138			Sequence 138, Ap
- 11	2146.5	86.9	475	4	US-10-225-810-41			Sequence 41, Appli
- 12	2139.5	86.7	475	4	US-10-225-810-18			Sequence 18, Appli
- 13	2137.5	86.6	475	4	US-10-225-810-18			Sequence 4, Appli
- 14	1914	77.5	422	4	US-10-291-731-4			Sequence 4, Appli
- 15	1914	77.5	422	4	US-10-165-564-4			Sequence 19, Appli
- 16	1722.5	69.8	483	4	US-10-225-810-19			Sequence 2, Appli
- 17	1718.5	69.6	483	4	US-10-392-219-2			Sequence 7, Appli
- 18	1718.5	69.6	507	4	US-10-167-685-7			Sequence 14, Appli
- 19	1606.5	68.7	478	4	US-10-225-810-14			Sequence 22, Appli
- 20	1677.5	67.9	481	4	US-10-225-810-22			Sequence 20, Appli
- 21	1476.5	59.8	470	4	US-10-225-810-20			Sequence 2, Appli
- 22	1448.5	58.7	427	4	US-10-165-564-2			Sequence 2, Appli
- 23	1448.5	58.7	427	4	US-10-165-564-2			Sequence 17, Appli
- 24	1416.5	57.4	477	4	US-10-225-810-17			Sequence 17, Appli
- 25	1263	51.2	263	4	US-10-080-334-24			Sequence 24, Appli
- 26	1255.5	50.9	485	4	US-10-055-055-2			Sequence 2, Appli
- 27	1255.5	50.9	485	4	US-10-154-419-92			Sequence 92, Appli

RESULT 2

US-10-225-810-21

Sequence 21, Application US/10225810

Publication No. US20030157512A1

GENERAL INFORMATION:

APPLICANT: Birmingham, Jr., John R.

TITLE OF INVENTION: Tramdorins and Methods of Using Tramdorin

FILE REFERENCE: McLaugh-07165

CURRENT APPLICATION NUMBER: US/10/225, 810

CURRENT FILING DATE: 2002-08-21

NUMBER OF SEQ ID NOS: 76

SOFTWARE: Patentin version 3.2

SEQ ID NO 21

LENGTH: 476

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-810-21

Query Match 100.0%; Score 2469; DB 4; Length 476;

Best Local Similarity 100.0%; Pred. No. 1.7e-217;

Matches 476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MSTQLRNEDYHDYSSTDVSPEESPSEGNNLSSPGSYORFGQSNSTTWQTLIHLKGN 60

Qy 1 MSTQLRNEDYHDYSSTDVSPEESPSEGNNLSSPGSYORFGQSNSTTWQTLIHLKGN 60

Db 1 MSTQLRNEDYHDYSSTDVSPEESPSEGNNLSSPGSYORFGQSNSTTWQTLIHLKGN 60

Qy 61 IGTGLGLPLAVKNAGIIMGPISLIIIGIVAHCMGLVYKCAHFCRRLINKSFVDYGDTV 120

Db 61 IGTGLGLPLAVKNAGIIMGPISLIIIGIVAHCMGLVYKCAHFCRRLINKSFVDYGDTV 120

Qy 121 MYGLSSPCSWLRLNHAHGRVYDFLITQLGFCYYFVFLADNFKQVTEAANGTTNC 180

Db 121 MYGLSSPCSWLRLNHAHGRVYDFLITQLGFCYYFVFLADNFKQVTEAANGTTNC 180

Qy 181 HNNETVILTPMDRSLYMSLFPFLVLFIRNLRLSIFSLLANITMVLSLMIQFLV 240

Db 181 HNNETVILTPMDRSLYMSLFPFLVLFIRNLRLSIFSLLANITMVLSLMIQFLV 240

Qy 241 QRPDPSHLPLVAPWKTYPPLFFGTAIPSSEGIMVLPLENKMDPRKFPLILYGMVYT 300

Db 241 QRPDPSHLPLVAPWKTYPPLFFGTAIPSSEGIMVLPLENKMDPRKFPLILYGMVYT 300

Qy 301 ILYISLGCGYLQFGANTQGTSITLNPNWLYQSVKLISIGIFTYTAQFYVPAELIP 360

Db 301 ILYISLGCGYLQFGANTQGTSITLNPNWLYQSVKLISIGIFTYTAQFYVPAELIP 360

Qy 361 FFVSRAPHECELYDLYDFRTVLVCLTCILAILPRDLIVSLSVSSSALLIIPPLIE 420

Db 361 FFVSRAPHECELYDLYDFRTVLVCLTCILAILPRDLIVSLSVSSSALLIIPPLIE 420

Qy 421 VTFYSEGSMSPLTIFKDALISLGFVGFVYGTYEALYELIOPSNAPIINSTCAFI 476

Db 421 VTFYSEGSMSPLTIFKDALISLGFVGFVYGTYEALYELIOPSNAPIINSTCAFI 476

Qy 241 QRPDPSHLPLVAPWKTYPPLFFGTAIPSSEGIMVLPLENKMDPRKFPLILYGMVYT 300

Db 241 QRPDPSHLPLVAPWKTYPPLFFGTAIPSSEGIMVLPLENKMDPRKFPLILYGMVYT 300

Qy 301 ILYISLGCGYLQFGANTQGTSITLNPNWLYQSVKLISIGIFTYTAQFYVPAELIP 360

Db 301 ILYISLGCGYLQFGANTQGTSITLNPNWLYQSVKLISIGIFTYTAQFYVPAELIP 360

Qy 361 FFVSRAPHECELYDLYDFRTVLVCLTCILAILPRDLIVSLSVSSSALLIIPPLIE 420

Db 361 FFVSRAPHECELYDLYDFRTVLVCLTCILAILPRDLIVSLSVSSSALLIIPPLIE 420

Qy 421 VTFYSEGSMSPLTIFKDALISLGFVGFVYGTYEALYELIOPSNAPIINSTCAFI 476

Db 421 VTFYSEGSMSPLTIFKDALISLGFVGFVYGTYEALYELIOPSNAPIINSTCAFI 476

RESULT 3

US-10-679-362-2

Sequence 2, Application US/10679362

Publication No. US20040146887A1

GENERAL INFORMATION:

APPLICANT: Wei, Ming Hui

TITLE OF INVENTION: NUCLEAR ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS, AND USES THEREOF

FILE REFERENCE: C1001062CON

CURRENT APPLICATION NUMBER: US/10/679, 362

RESULT 4

US-10-080-334-22

Sequence 22, Application US/10080334

Publication No. US20040002584A1

GENERAL INFORMATION:

APPLICANT: Pena, Carol E. A.

APPLICANT: Shimkets, Richard A.

APPLICANT: Li, Li

APPLICANT: Shenoy, Sureesh G

APPLICANT: Kekuda, Ramesh

APPLICANT: Spivak, Kimberly A.

APPLICANT: Vernet, Corinne A. M.

APPLICANT: Malyantar, Uriel M

APPLICANT: Guo, Xiaojia

APPLICANT: Gusev, Vladimir Y

APPLICANT: Casman, Stacie J

APPLICANT: Boldog, Ferenc L

APPLICANT: Furuk, Katarzyna T

APPLICANT: Tchernev, Velizar T

APPLICANT: Patturajan, Meera

APPLICANT: Ganguli, Esha A

APPLICANT: Padigaru, Muralidhara

APPLICANT: Baungartner, Jason C.

APPLICANT: Gerlach, Valerie

APPLICANT: Spaderna, Steven K

APPLICANT: Zerhusen, Bryan D

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
 TITLE OF INVENTION: Using the Same  
 FILE REFERENCE: 214 02-275  
 CURRENT APPLICATION NUMBER: US10/080,334  
 FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 60/270,523  
 PRIOR FILING DATE: 2001-02-21  
 PRIOR APPLICATION NUMBER: 60/322,712  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: 60/311,980  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: 60/330,307  
 PRIOR FILING DATE: 2001-10-18  
 PRIOR APPLICATION NUMBER: 60/278,796  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/281,521  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/276,677  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/311,595  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: 60/270,220  
 PRIOR FILING DATE: 2001-02-21  
 PRIOR APPLICATION NUMBER: 60/274,295  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: 60/318,526  
 PRIOR FILING DATE: 2001-09-10  
 PRIOR APPLICATION NUMBER: 60/286,548  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: 60/291,765  
 PRIOR FILING DATE: 2001-05-17  
 PRIOR APPLICATION NUMBER: 60/270,797  
 PRIOR FILING DATE: 2001-02-23  
 PRIOR APPLICATION NUMBER: 60/276,400  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/270,810  
 PRIOR FILING DATE: 2001-02-23  
 NUMBER OF SEQ ID NOS: 388  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 22  
 LENGTH: 496  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-080-334-22

Query Match 99.6%; Score 2460; DB 4; Length 496;  
 Best Local Similarity 99.6%; Pred. No. 1.2e-216;  
 Matches 475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSTQRNEDYDYSSTDVSDEEPSEGNNLSSPSSYQRGQSNSTTWQTLILKGN 60

Db 21 MSTQRNEDYDYSSTDVSDEEPSEGNNLSSPSSYQRGQSNSTTWQTLILKGN 80

Qy 61 1GTGLGLPLAVKNAQIVMGPSLTLIGIVAHCMGILVCAHHFCRRLNSFVDYGDTV 120

Db 81 1GTGLGLPLAVKNAQIVMGPSLTLIGIVAHCMGILVCAHHFCRRLNSFVDYGDTV 140

Qy 121 MYGLESSPCSNLRRNHAHMGREVDFFLVTOLGFCCVYFVLADNPKQVTEAANGTNNC 180

Db 141 MYGLESSPCSNLRRNHAHMGREVDFFLVTOLGFCCVYFVLADNPKQVTEAANGTNNC 200

Qy 181 HNNETVLTPTMDSRLYMLSPFLVILVFRNLRLSISLLANITMLSLVMIYQFIV 240

Db 201 HNNETVLTPTMDSRLYMLSPFLVILVFRNLRLSISLLANITMLSLVMIYQFIV 260

Qy 241 QRIDPSHLPLVAPWKTPLFFGTAIFSFEGIGMVLPLENKMDPKPKPLLYLGTV 300

Db 261 QRIDPSHLPLVAPWKTPLFFGTAIFSFEGIGMVLPLENKMDPKPKPLLYLGTV 320

Qy 301 ILYISIGCLGVLQFGANIQGSITLNLUPNCMLYQSVKLILSISIFFTYALQFVPAEIIIP 360

Db 321 ILYISIGCLGVLQFGANIQGSITLNLUPNCMLYQSVKLILSISIFFTYALQFVPAEIIIP 380

RESULT 5  
 US-10-332-447-8  
 ; Sequence 8, Application US10332447  
 ; Publication No. US20040053258A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE GENOMICS, INC.; RAIMANN, Brigitte E.;  
 ; APPLICANT: THORNTON, Michael; DING, Li; YUE, Henry;  
 ; APPLICANT: TANG, Y. Tom; HARLAND, Lee; BURFORD, Neil;  
 ; APPLICANT: GREENE, Barrie D.; SANJANWALA, Madhu S.;  
 ; APPLICANT: BAUGHN, Mariah R.; YAO, Monique G.; YANG, Junming;  
 ; APPLICANT: ARVALZU, Chandra S.; GANDHI, Ameena R.;  
 ; APPLICANT: HAFALIA, April J.A.; TRBOULEY, Catherine M.;  
 ; APPLICANT: WALTA, Narinder K.; AU-YOUNG, Janice;  
 ; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Jayalaxmi;  
 ; APPLICANT: LU, Yan; LU, Duyng Aina M.; AZIMZAI, Yalda;  
 ; APPLICANT: XU, Yuming; ELLIHAMER, Vicki S.; DANIEL B.;  
 ; APPLICANT: XU, Yuming; SETLHAMER, Jeffrey J.; BOROWSKY, Mark L.;  
 ; APPLICANT: KHAN, Farrah A.; KEARNEY, Liam; THANGAVELU, Kavitha;  
 ; APPLICANT: DAS, Debopriya; POLICKY, Jennifer L.;  
 ; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS  
 ; FILE REFERENCE: PI-0149 USN  
 ; CURRENT APPLICATION NUMBER: US 10/332,447  
 ; CURRENT FILING DATE: 2003-01-07  
 ; PRIOR APPLICATION NUMBER: US 60/216,547  
 ; PRIOR FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/218,232  
 ; PRIOR FILING DATE: 2000-07-14  
 ; PRIOR APPLICATION NUMBER: US 60/220,112  
 ; PRIOR FILING DATE: 2000-07-21  
 ; PRIOR APPLICATION NUMBER: US 60/221,839  
 ; PRIOR FILING DATE: 2000-07-28  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO: 8  
 ; LENGTH: 568  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. US20040053258A1 7476747CD1  
 US-10-332-447-8

Query Match 97.3%; Score 2402.5;  
 Best Local Similarity 88.3%; Pred. No. 2.6e-211;  
 Matches 474; Conservative 0; Mismatches 2; Indels 61; Gaps 2;

Qy 1 MSTQRNEDYDYSSTDVSDEEPSEGNNLSSPSSYQRGQSNSTTWQTLILKGN 60

Db 32 MSTQRNEDYDYSSTDVSDEEPSEGNNLSSPSSYQRGQSNSTTWQTLILKGN 91

Qy 61 1GTGLGLPLAVKNAQIVMGPSLTLIGIVAHCMGILVCAHHFCRRLNSFVDYGDTV 120

Db 92 1GTGLGLPLAVKNAQIVMGPSLTLIGIVAHCMGILVCAHHFCRRLNSFVDYGDTV 151

Qy 121 MYGLESSPCSNLRRNHAHMGREVDFFLVTOLGFCCVYFVLADNPKQVTEAANGTNNC 180

Db 152 MYGLESSPCSNLRRNHAHMGREVDFFLVTOLGFCCVYFVLADNPKQVTEAANGTNNC 211

Qy 181 HNNETVLTPTMDSRLYMLSPFLVILVFRNLRLSISLLANITMLSLVMIYQFIV 240

Db 212 HNNETVLTPTMDSRLYMLSPFLVILVFRNLRLSISLLANITMLSLVMIYQFIV 271

Qy 241 QRIDPSHLPLVAPWKTPLFFGTAIFSFEGIGMVLPLENKMDPKPKPLLYLGTV 300

Db 241 QRIDPSHLPLVAPWKTPLFFGTAIFSFEGIGMVLPLENKMDPKPKPLLYLGTV 300

Db 2772 QRIPPSHLPLVAPWKTYPPLFFGTAIFSEGGMVLPLENKMKDPRKFPLILYLGMIYT 331 ; PRIOR APPLICATION NUMBER: 60/286,548  
 Qy 301 ILYISLGCGCYLQGANIQSITINLPNCWLYQSYKLILSIGGIFTYALQFYPAEITP 360 ; PRIOR FILING DATE: 2001-04-25  
 Db 332 ILYISLGCGCYLQGANIQSITINLPNCWLYQSYKLILSIGGIFTYALQFYPAEITP 391 ; PRIOR APPLICATION NUMBER: 60/291,765  
 Qy 361 FFVSSRAPEHCELYVVDLFVTVLVCUT-----386 ; PRIOR FILING DATE: 2001-05-17  
 Db 392 FFVSSRAPEHCELYVVDLFVTVLVCUTSLSGSVDNGWYGEADGTSGCASPPLVPSSSFA 451 ; PRIOR APPLICATION NUMBER: 60/270,810  
 Qy 387 -----C-----I-LAIIPLRDLVLSVGSVSSALIIPPL 419 ; PRIOR FILING DATE: 2001-02-23  
 Db 452 HPWLSFRCEQSOWVSCHRTVVWGFARGILAIPLRDLVLSVGSVSSALIIPPL 511 ; NUMBER OF SEQ ID NOS: 388  
 Qy 420 EVTTYSEGNSPLTIFKDALIISTIGFVGTVGTYEALYLQELIOPSNAPINSTCAFI 476 ; SOFTWARE: PatentIn Ver. 2.1  
 Db 512 EVTTYSEGNSPLTIFKDALIISLGFGVFGTVGTYEALYLQELIOPSNAPINSTCAFI 568 ; SEQ ID NO: 20  
 ; LENGTH: 500  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-080-334-20

---

Query Match 97.1%; Score 2398; DB 4; Length 500;  
 Best Local Similarity 97.5%; Pred: No. 5.8e-211;  
 Matches 472; Conservative 0; Missmatches 0; Index 12; Gaps 3;

Qy 1 M\$TQRLRNEDYHDYSSTDVSPPEESPSEGINNLSSP\$Y\$ORGNSNTTWFQTLIHLRKGN 60  
 Db 21 M\$TQRLRNEDYHDYSSTDVSPPEESPSEGINNLSSP\$Y\$ORGNSNTTWFQTLIHLRKGN 80

Qy 61 IGTGLGLPLAVKAGIIGMPISLILIGIVAVICMGLILYKCAHFCRRLINKSFYDYGDTV 120  
 Db 81 IGTGLGLPLAVKAGIIGMPISLILIGIVAVICMGLILYKCAHFCRRLINKSFYDYGDTV 140

Qy 121 MYGLESSPCSWLNHNAHGRVVDFLITVOLGFCCYVFVLADNFKVOIEAANGTTNCC 180  
 Db 141 MYGESSPCSWLNHNAHGRVVDFLITVOLGFCCYVFVLADNFKVOIEAANGTTNCC 200

Qy 181 HNNETVILTPMDSRILYMLSFLPFLVILVFNRLAITSFSLIANTIMLVSLYM1YQFIV 240  
 Db 201 HNNETVILTPMDSRILYMLSFLPFLVILVFNRLAITSFSLIANTIMLVSLYM1YQFIV 260

Qy 241 -----ORIPDSHLPVAPWKTYPPLFFGTAIFSSPEGIMVLPLENKMDPKFPLIL 292  
 Db 261 FRYMLSVFRIPDPSHLPVAPWKTYPPLFFGTAIFSSPEGIMVLPLENKMDPKFPLIL 320

Qy 293 YLGMVIVTLYISLGCLGYLQFGANIQGSITILNPNCWLYQSVKLILSTGIFTYALQPY 352  
 Db 321 YLGRVIVTLYISLGCLGYLQFGANIQGSITILNPNCWLYQSVKLILSTGIFTYALQPY 377

Qy 353 VPARIIIPFFVSRAPHECBLVVDLFVRTVLCUTCLTALIPLRDVLSVGSYSSALA 412  
 Db 378 VPARIIIPFFVSRAPHECBLVVDLFVRTVLCUT-ILALIPLRDVLSVGSYSSALA 436

Qy 413 LIIPPLLETTFSEGMSLTIKDALISLGFGVFGTYEALYLQELIOPSNAPINST 472  
 Db 437 LIIPPLLETTFSEGMSLTIKDALISLGFGVFGTYEALYLQELIOPSNAPINST 496

Qy 473 CAFI 476  
 Db 497 CAFI 500

RESULT 7  
 US-09-805-456-7  
 ; Sequence 7, Application US/09805456  
 ; Public No. US20030170778A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEI, Ming-Hui  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: AND USES THEREOF  
 ; FILE REFERENCE: C1001062  
 ; CURRENT APPLICATION NUMBER: US/09/805,456  
 ; CURRENT FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: 60/270,523  
 ; PRIOR FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: 60/322,712  
 ; PRIOR FILING DATE: 2001-09-17  
 ; PRIOR APPLICATION NUMBER: 60/311,980  
 ; PRIOR FILING DATE: 2001-08-13  
 ; PRIOR APPLICATION NUMBER: 60/330,307  
 ; PRIOR FILING DATE: 2001-10-18  
 ; PRIOR APPLICATION NUMBER: 60/278,796  
 ; PRIOR FILING DATE: 2001-03-26  
 ; PRIOR APPLICATION NUMBER: 60/281,521  
 ; PRIOR FILING DATE: 2001-04-04  
 ; PRIOR APPLICATION NUMBER: 60/276,677  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: 60/311,595  
 ; PRIOR FILING DATE: 2001-08-10  
 ; PRIOR APPLICATION NUMBER: 60/270,220  
 ; PRIOR FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: 60/274,295  
 ; PRIOR FILING DATE: 2001-03-08  
 ; PRIOR APPLICATION NUMBER: 60/318,526  
 ; PRIOR FILING DATE: 2001-09-10  
 ; SOFTWARE: FastSEQ For Windows Version 4.0

SEQ ID NO 7  
 LENGTH: 476  
 TYPE: PRT  
 ORGANISM: Human  
 US-09-805-456-7

Query Match 94.1%; Score 2324; DB 3; Length 476;  
 Best Local Similarity 94.5%; Pred. No. 3.3e-204;  
 Matches 450; Conservative 9; Mismatches. 17; Indels 0; Gaps 0;

Qy 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60  
 Db 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60

Qy 61 1GTGLLGLPLAVKNAGITVMGPISLTLIGIVAVHCMGILVKCAHHFTRLANKSFVDYGDTV 120  
 Db 61 1GTGLLGLPLAVKNAGITVMGPISLTLIGIVAVHCMGILVKCAHHFTRLANKSFVDYGDTV 120

Qy 121 MYGLESSPCSWLRNHHAWGRVDFPLVFLVFLRNLALSIFSLANITMVLSSVLYQFIV 180  
 Db 121 MYGLESSPCSWLRNHHAWGRVDFPLVFLVFLRNLALSIFSLANITMVLSSVLYQFIV 180

Qy 181 HNNETVLTPTMDSLYMLSLPFLVFLVFLRNLALSIFSLANITMVLSSVLYQFIV 240  
 Db 181 HNNETVLTPTMDSLYMLSLPFLVFLVFLRNLALSIFSLANITMVLSSVLYQFIV 240

Qy 241 QRIDPSHSLPLAVPKTYPLFPGTAIFSEGIGMVLPLENKMDPRKFPLILYLGIVVT 300  
 Db 241 QRIDPSHSLPLAVPKTYPLFPGTAIFSEGIGMVLPLENKMDPRKFPLILYLGIVVT 300

Qy 301 ILYISIGCLGYLQFGANIQSITLNLPNCWLYQSVKLLYSIGIFFTYALQYVPAELIIP 360  
 Db 301 ILYISIGCLGYLQFGANIQSITLNLPNCWLYQSVKLLYSIGIFFTYALQYVPAELIIP 360

Qy 361 FFVFSRAPEHCELVVDLFLVRLTVLCLATLIPRLDVLISVGSSSALALIIPPLE 420  
 Db 361 VIVSWWCKCCTLMVDLGIGSAMLCKTCITLIPRLDVLISVGSSSALALIIPPLE 420

Qy 421 VTTFSEGMSPLTIFKDALISLGFVGFVGTYEALYELIOPSNAPIFINSTCAFI 476  
 Db 421 VTTFSEGMSPLTIFKDALISLGFVGFVGTYEALYELIOPSNAPIFINSTCAFI 476

RESULT 9  
 US-10-094-749-3076  
 Sequence 3076, Application US/10094749  
 Publication No. US20030219741A1  
 GENERAL INFORMATION:  
 APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: OTSUKI, TETSUJI  
 APPLICANT: WAKANAKI, AI  
 APPLICANT: SATO, HIROYUKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMECHIKA, ICHIRO  
 APPLICANT: SEKI, NAOKI  
 APPLICANT: YOSHIKAWA, TSUTOMU  
 APPLICANT: OTSUKA, MOTOKI  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: MASUO, YASUHIKO  
 TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA  
 FILE REFERENCE: 084335/0160  
 CURRENT APPLICATION NUMBER: US/10/094,749  
 CURRENT FILING DATE: 2002-03-12  
 PRIOR APPLICATION NUMBER: 60/350,435  
 PRIOR FILING DATE: 2000-01-24  
 PRIOR APPLICATION NUMBER: JP 2001-328381  
 PRIOR FILING DATE: 2001-09-14  
 NUMBER OF SEQ ID NOS: 3381  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 7  
 LENGTH: 476  
 TYPE: PRT  
 ORGANISM: Human  
 US-10-679-362-7

Query Match 94.1%; Score 2324; DB 4; Length 476;  
 Best Local Similarity 94.5%; Pred. No. 3.3e-204;  
 Matches 450; Conservative 9; Mismatches. 17; Indels 0; Gaps 0;

Qy 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60  
 Db 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60

Qy 61 1GTGLLGLPLAVKNAGITVMGPISLTLIGIVAVHCMGILVKCAHHFTRLANKSFVDYGDTV 120  
 Db 61 1GTGLLGLPLAVKNAGITVMGPISLTLIGIVAVHCMGILVKCAHHFTRLANKSFVDYGDTV 120

Query Match 89.8%; Score 2217; DB 4; Length 434;  
 Best Local Similarity 90.8%; Pred. No. 1.9e-194;  
 Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;  
 SEQ ID NO 7  
 LENGTH: 434  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-094-749-3076

Query Match 89.8%; Score 2217; DB 4; Length 434;  
 Best Local Similarity 90.8%; Pred. No. 1.9e-194;  
 Matches 432; Conservative 1; Mismatches 1; Indels 42; Gaps 1;  
 SEQ ID NO 7  
 LENGTH: 434  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-094-749-3076

Qy 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60  
 Db 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60

Qy 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60  
 Db 1 MSTQRNEDYHDYSSTDSPEESPSEGNNLSSPSSYQRFGQSNTTWFOTLHILKGN 60

RESULT 10  
US-10-080-334-137

Sequence 137, Application US/10080334  
Publication No. US20040002384A1  
GENERAL INFORMATION:  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Shimitkis, Richard A  
APPLICANT: Li, Li  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spyrek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Guo, Xiaojia  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Furcak, Katarzyna  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Patterajan, Meera  
APPLICANT: Gangoli, Esha A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Liu, Xiaohong  
APPLICANT: Baungartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
TITLE OF INVENTION: Using the Same  
FILE REFERENCE: 214 02-275  
CURRENT APPLICATION NUMBER: US/10/080,334  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/210,523  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/322,712  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/311,980  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/330,307  
PRIOR FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 60/278,796  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/281,521

RESULT 11  
US-10-080-334-138

Sequence 138, Application US/10080334  
Publication No. US20040002384A1  
GENERAL INFORMATION:  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Shimitkis, Richard A  
APPLICANT: Li, Li  
APPLICANT: Shenoy, Suresh G  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Spyrek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Malyankar, Uriel M  
APPLICANT: Guo, Xiaojia  
APPLICANT: Gusev, Vladimir Y  
APPLICANT: Casman, Stacie J  
APPLICANT: Boldog, Ferenc L  
APPLICANT: Furcak, Katarzyna  
APPLICANT: Tchernev, Velizar T  
APPLICANT: Patterajan, Meera  
APPLICANT: Gangoli, Esha A  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Liu, Xiaohong  
APPLICANT: Baungartner, Jason C.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Spaderna, Steven K  
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
TITLE OF INVENTION: Using the Same  
FILE REFERENCE: 214 02-275  
CURRENT APPLICATION NUMBER: US/10/080,334  
CURRENT FILING DATE: 2002-02-21  
PRIOR APPLICATION NUMBER: 60/210,523  
PRIOR FILING DATE: 2001-02-21  
PRIOR APPLICATION NUMBER: 60/322,712  
PRIOR FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: 60/311,980  
PRIOR FILING DATE: 2001-08-13  
PRIOR APPLICATION NUMBER: 60/330,307  
PRIOR FILING DATE: 2001-10-18  
PRIOR APPLICATION NUMBER: 60/278,796  
PRIOR FILING DATE: 2001-03-26  
PRIOR APPLICATION NUMBER: 60/281,521

APPLICANT: Li, Li  
 APPLICANT: Shenoy, Suresh G  
 APPLICANT: Kekuda, Ramesh  
 APPLICANT: Kimberly A.  
 APPLICANT: Vernet, Corine A. M.  
 APPLICANT: Malyankar, Uriel M.  
 APPLICANT: Guo, Xiaotia  
 APPLICANT: Gusev, Vladimir Y  
 APPLICANT: Casman, Stacie J  
 APPLICANT: Boldog, Ferenc L  
 APPLICANT: Furtek, Katerzyna T  
 APPLICANT: Tchernev, Velizar T  
 APPLICANT: Patturajan, Meera T  
 APPLICANT: Gangoli, Esha A  
 APPLICANT: Padigaru, Muralidhara  
 APPLICANT: Liu, Xiaohong  
 APPLICANT: Baungartner, Jason C.  
 APPLICANT: Gerlach, Valerie  
 APPLICANT: Spaderna, Steven K  
 APPLICANT: Zernusen, Bryan D

TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of  
 TITLE OF INVENTION: Using the Same  
 FILE REFERENCE: 214 02-275

CURRENT APPLICATION NUMBER: US/10/080,334  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 60/270,523  
 PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/322,712  
 PRIOR FILING DATE: 2001-09-17  
 PRIOR APPLICATION NUMBER: 60/311,980  
 PRIOR FILING DATE: 2001-08-13  
 PRIOR APPLICATION NUMBER: 60/330,307  
 PRIOR FILING DATE: 2001-10-18  
 PRIOR APPLICATION NUMBER: 60/278,796  
 PRIOR FILING DATE: 2001-03-26  
 PRIOR APPLICATION NUMBER: 60/281,521  
 PRIOR FILING DATE: 2001-04-04  
 PRIOR APPLICATION NUMBER: 60/276,677  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/311,595  
 PRIOR FILING DATE: 2001-08-10  
 PRIOR APPLICATION NUMBER: 60/270,220  
 PRIOR FILING DATE: 2001-02-21  
 PRIOR APPLICATION NUMBER: 60/274,295  
 PRIOR FILING DATE: 2001-03-08  
 PRIOR APPLICATION NUMBER: 60/318,526  
 PRIOR FILING DATE: 2001-09-10  
 PRIOR APPLICATION NUMBER: 60/286,548  
 PRIOR FILING DATE: 2001-04-25  
 PRIOR APPLICATION NUMBER: 60/291,765  
 PRIOR FILING DATE: 2001-05-17  
 PRIOR APPLICATION NUMBER: 60/270,797  
 PRIOR FILING DATE: 2001-02-23  
 PRIOR APPLICATION NUMBER: 60/275,400  
 PRIOR FILING DATE: 2001-03-16  
 PRIOR APPLICATION NUMBER: 60/270,810  
 NUMBER OF SEQ ID NOS: 388  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 138  
 LENGTH: 475  
 TYPE: PRT  
 ORGANISM: Rattus norvegicus  
 US-10-080-334-138

Query Match 86.9%; Score 2146.5; DB 4; Length 475;  
 Best Local Similarity 85.7%; Pred. No. 6.3e-188; Mismatches 36; Indels 1; Gaps 1;

Db 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 60  
 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 59

Db 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 60  
 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 59

Qy 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 60  
 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 59

Db 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 60  
 1 M70QRLRNEDYHDSSSTDVSPEESPESEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 59

Qy 61 IGTGLIGLPLAVKNAGIVMGPISLJLJIGIVAHCMGLVYKCAHHRCCRRLINKSFVVDYGDPTV 120  
 60 IGTGLIGLPLAVKNAGLILGPSPSLIVIGIVAHCMGLVYKCAHHRCCRRLINKPFLDYGDTV 119

Db 121 MYGLLESSPCSWLRLNAHMGRRVVDPEFLIVTOLGFCCVYFLADNPKVIEAANGTTNNC 180  
 120 MYGLLESSPCSWLRLNAHMGRRVVDPEFLIVTOLGFCCVYFLADNPKVIEAANGTTNNC 179

Qy 181 HNNETVILTPMDSYLMLSPFLPFLVLLPFLRNALSISLLANITMLVSLVMYQFIV 240  
 180 HNNETVILTPMDSYLMLSPFLPFLVLLPFLRNRLSISLLANISMFVSLIMYQFIV 239

Db 180 NNNETVILTPMDSYLMLSPFLPFLVLLPFLRNRLSISLLANISMFVSLIMYQFIV 239  
 180 NNNETVILTPMDSYLMLSPFLPFLVLLPFLRNRLSISLLANISMFVSLIMYQFIV 239

Qy 241 QRIDPDSHLPLIVAPKNTYPLFFGTAIFSEPGMVLPLENRMKDPRKFLPLLYGIVVIT 300  
 240 QRIDPDSHLPLIVAPKNTYPLFFGTAIFSEPGMVLPLENRMKDPRKFLPLLYGIVVIT 299

Db 240 QRIDPDSHLPLIVAPKNTYPLFFGTAIFSEPGMVLPLENRMKDPRKFLPLLYGIVVIT 299  
 240 QRIDPDSHLPLIVAPKNTYPLFFGTAIFSEPGMVLPLENRMKDPRKFLPLLYGIVVIT 299

Qy 301 ILYISLIGLGLQFGANIQSITNLPNCMLYQSYKLISIGIIFTYALQFYVPAEIIIP 360  
 300 VLYISLGSLGYQFADIGSITNLPNCMLYQSYKLISIGIIFTYALQFYVAEIIIP 359

Db 361 FFVSRAPHECBLVVFLFVRLVLCUTCILALIPFLDVLVSGVYSSSALLIPPLLE 420  
 360 AIVSRVPEREFLVLDLTSRPMVCTVLAVLIPRLDVLVSGVYSSSALLIPPLLE 419

Qy 421 VTFYSEGMSPLTIPKDALISLGTVFVGTYEALIOPSNAPIFINSTCAFI 476  
 420 VTFYGEIGSPLTIPKDALISLGTVFVGTYEBSLWELIOPSHSDSSTNSTSAFI 475

RESULT 12  
 US-10-225-810-41  
 ; Sequence 41, Application US/10225810  
 ; Publication No. US2003015712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Birmingham, Jr., John R.  
 ; TITLE OF INVENTION: Tramordin and Methods of Using Tramordin  
 ; FILE REFERENCE: McLaugh-01165  
 ; CURRENT APPLICATION NUMBER: US/10/225,810  
 ; CURRENT FILING DATE: 2002-08-21  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO: 41  
 ; LENGTH: 475  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 ; US-10-225-810-41

Query Match 86.7%; Score 2139.5; DB 4; Length 475;  
 Best Local Similarity 85.3%; Pred. No. 2.8e-187; Mismatches 37; Indels 1; Gaps 1;

Db 1 M70QRLRNEDYHDSSSTDVSPEESSEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 60  
 1 M70QRLRNEDYHDSSSTDVSPEESSEGILNLSSPSSYQRFQGSNSTTWFTLILKGN 59

Qy 61 IGTGLIGLPLAVKNAGIVMGPISLJLJIGIVAHCMGLVYKCAHHRCCRRLINKSFVVDYGDPTV 120  
 60 IGTGLIGLPLAVKNAGLILGPSPSLIVIGIVAHCMGLVYKCAHHRCCRRLINKPFLDYGDTV 119

Db 121 MYGLLESSPCSWLRLNAHMGRRVVDPEFLIVTOLGFCCVYFLADNPKVIEAANGTTNNC 180  
 120 MYGLLESSPCSWLRLNAHMGRRVVDPEFLIVTOLGFCCVYFLADNPKVIEAANGTTNNC 179

Qy 181 HNNETVILTPMDSYLMLSPFLPFLVLLPFLRNALSISLLANITMLVSLVMYQFIV 240  
 180 NNNETVILTPMDSYLMLSPFLPFLVLLPFLRNRLSISLLANISMFVSLIMYQFIV 239

RESULT 13  
 US-10-225-810-18  
 ; Sequence 18, Application US/10225810  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bermingham, Jr., John R.  
 ; TITLE OF INVENTION: Tramdorin and Methods of Using Tramdorin  
 ; FILE REFERENCE: McLaugh-07165  
 ; CURRENT APPLICATION NUMBER: US/10/225, 810  
 ; CURRENT FILING DATE: 2002-08-21  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 18  
 ; LENGTH: 475  
 ; TYPE: PRT  
 ; ORGANISM: Mus musculus  
 ; US-10-225-810-18

Query Match 86.6%; Score 2137.5; DB 4; Length 475;  
 Best Local Similarity 85.9%; Pred. No. 4.2e-187; Indels 1; Gaps 1;  
 Matches 409; Conservative 32; Mismatches 34; Delins 1; Gaps 1;

Db 1 MSTRQLRNEDYHDYDSSTSDDPEESPESEGNNLSSPGSDFRGQSNSTWMFQTLIHLKGN 60  
 Db 1 MSTRQLRNEDYHDYDSSTSDDPEESPESEGGSF-SPGSDFRGQSNSTWMFQTLIHLKGN 59

Qy 1 IGTGHGLPLAVKNAQIGIVMGPISLIIIGTAVHMGILKCAHFCRRLANKSFVYDGTW 120  
 Db 60 IGTGHGLPLAVKNAQGLLGPLSLIVIGTAVHMGILKCAHFCRRLANKPFLDYGDTW 119

Qy 121 MYGLESSPCSWLNRFAHWRGRVDFLITVQLGFCCVYTVFLADNFQKVEAANGTTNC 180  
 Db 120 MYGLECSPSTWVRNFSHWRGRVDFLITVQLGFCCVYTVFLADNFQKVEAANGTTNC 179

Qy 181 HNNETVILTPMDSRSLYML-SFLPFLVLLYFIRNLRLSFSLLANITMLVSLLMIYQFV 240  
 Db 180 NNNNTVVIPTMDSRSLYMPFLPFLVLLYFIRNLRLSFSLLANISMSLIMIYQFV 239

Qy 241 QRIDPDSHPLVAPKTKYPLFFGTAIFSEPGIGVLPFLNKMDQPRKFPLILGMVIT 300  
 Db 240 QRIDPDSHPLVAPKTKYPLFFGTAIFSEPGIGVLPFLNKMDQKFPLILGMVIT 299

Qy 301 LYISLGCGLYLOFANIGQSIITANLPNCWLYQSVLNSIGIFFTYALQYPAEILIP 360  
 Db 300 VLYISLGSGLYLOFANIGQSIITANLPNCWLYQSVLNSIGIFFTYALQYPAEILIP 359

Qy 361 FFVSRAPHECELWVDFRVTVLVCLTCIAILIPRLDVLSGSVSSALALIIPPLE 420  
 Db 360 AIVSRVPERHECELWVDFRVTVCVAMVCVTLVPLRDLVLSGSVSSALALIIPPLE 419

Qy 421 VTTFSEGMSPLTIFKDALISILGFVGFVGTYALVELIQPSNAPIFINSTCAFI 476  
 Db 420 VVTYYGEGISPLTIVTKDALISILGFVGFVGTYELQPSHSDSSNTNSAFI 475

RESULT 14  
 US-10-291-737-4  
 ; Sequence 4, Application US/10291737  
 ; Publication No. US20030087299A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; FILE REFERENCE: CLO0101-1-CIPCON  
 ; CURRENT FILING DATE: 2003-02-13  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO 4

RESULT 15  
 US-10-365-564-4  
 ; Sequence 4, Application US/10365564  
 ; Publication No. US2003013623A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: WEBSTER, Marion et al.  
 ; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,  
 ; FILE REFERENCE: CLO0101-1-CIPCON  
 ; CURRENT APPLICATION NUMBER: US/10/365, 564  
 ; PRIOR APPLICATION NUMBER: US 09/822, 859  
 ; PRIOR FILING DATE: 2000-04-02  
 ; PRIOR APPLICATION NUMBER: US 60/254, 588  
 ; PRIOR FILING DATE: 2000-12-12  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSEQ For Windows Version 4.0  
 ; SEQ ID NO 4

```

; LENGTH: 422
; TYPE: PRT
; ORGANISM: Human
US-10-365-564-4

Query Match 77.5%; Score 1914; DB 4; Length 422;
Best Local Similarity 86.0%; Pred. No. 1.1e-166; Mismatches 33; Indels 0; Gaps 0;
Matches 363; Conservative 33; Mismatches 26; Indels 0; Gaps 0;

Qy 51 QTLIHLKGNTGTGLGLPLAKVAGIVMGPSLILIGIVAHCMGILVCAHHFRRIN 110
Db 1 QTLIHLKGNTGTGLGLPLAKVAGIVMGPSLILIGIVAHCMGILVCAHHFRRIN 60

Qy 111 KSFVDYGDITMYGLERSSPCSWLRLNHAHGRVYDPLFLITVOLGFCCVYFVFLADNEKQVI 170
Db 61 KPFLDYGDITMYGLECSPSTWRNHSWGRRIIVDFLFLVTVQLGFCVVYFVFLADNEKQVI 120

Qy 171 EAANGTTNCHNNETVLTPTMDSRAYMLSPFLVLFVFLNRLSISFELLANTMVLV 230
Db 121 EAANGTTNCHNNETVLTPTMDSRAYMLSPFLVLFVFLNRLSISFELLANISMFV 180

Qy 231 SLIMIYQFIVORIPDPSHLPLVAPWKTYPFLFGTAIFSFEGIGMVLPLENRKMDPRKFPL 290
Db 181 SLIMIYQFIVORIPDPSHLPLVAPWKTYPFLFGTAIFSFEGIGMVLPLENRKMDGKFPPL 240

Qy 291 ILYLGWVIVTLYISLGCLGLQFGGANIQGSITLNLPNCWLYQSYKLLISGIGFSTYALQ 350
Db 241 ILYLGWVITLYISLGSLGYLQFGADIKGSITLNIPNCWLYQSYKLLISGIGFSTYALQ 300

Qy 351 FYVPAELIIPFFVSRAPHECELVVDLFLVRLTCILATLIPRLDVLISLGVSYSSA 410
Db 301 FYVAAEITIPATIVSRVPERFLVVDLSARTAMVCITCVALVLPRLDVLISLGVSYSSA 360

Qy 411 LALIIIPPLETTFYSEGMSPLTIFKDALISLILGFVGVGTYEALYELIOPSNAPILPIN 450
Db 361 LALIIIPPLKVTTYGEGISPLTIXKDALISLILGFVGVGTYEALYELIOPSHSDSSTN 420

Qy 471 ST 472
Db 421 ST 422

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Search completed: August 24, 2006, 01:29:45  
 Job time : 186 secs

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Result No.	Score	Query	Match	Length	DB	ID	Description
1	1255.5	50.9	504	6	US-10-505-928-42	Sequence 42, App1	Sequence 42, Application US-10-505-928-42
2	972.5	39.4	369	7	US-11-293-697-3609	Sequence 3609, App	Sequence 3609, Application US-10-505-928-42
3	465.5	18.9	436	6	US-10-953-349-368	Sequence 368, App	Sequence 368, Application US-10-505-928-42
4	410.5	16.6	371	6	US-10-953-149-365	Sequence 369, App	Sequence 369, Application US-10-505-928-42
5	405	16.4	425	6	US-10-449-902-3701	Sequence 3701, A	Sequence 3701, Application US-10-505-928-42
6	405	16.4	425	6	US-10-449-902-49196	Sequence 4916, A	Sequence 4916, Application US-10-505-928-42
7	404.5	16.4	422	6	US-10-449-902-32842	Sequence 32842, A	Sequence 32842, Application US-10-505-928-42
8	404.5	16.4	422	6	US-10-449-902-32552	Sequence 32552, A	Sequence 32552, Application US-10-505-928-42
9	402.5	16.3	422	6	US-10-449-902-53486	Sequence 53486, A	Sequence 53486, Application US-10-505-928-42
10	400	16.2	395	6	US-10-449-902-22524	Sequence 29224, A	Sequence 29224, Application US-10-505-928-42
11	382	15.5	395	6	US-10-953-349-370	Sequence 370, App	Sequence 370, Application US-10-505-928-42
12	339.5	13.8	342	6	US-10-449-902-32686	Sequence 32686, A	Sequence 32686, Application US-10-505-928-42
13	332	13.4	349	6	US-10-449-902-36917	Sequence 36917, A	Sequence 36917, Application US-10-505-928-42
14	318	12.9	531	7	US-11-174-307B-5170	Sequence 5170, App	Sequence 5170, Application US-10-505-928-42
15	302	12.2	468	7	US-11-056-355B-105677	Sequence 105677, A	Sequence 105677, Application US-10-505-928-42
16	302	12.2	468	7	US-11-056-355B-116916	Sequence 116916, A	Sequence 116916, Application US-10-505-928-42
17	302	12.2	474	7	US-11-056-355B-105676	Sequence 105676, A	Sequence 105676, Application US-10-505-928-42
18	302	12.2	474	7	US-11-056-355B-116915	Sequence 116915, A	Sequence 116915, Application US-10-505-928-42
19	302	12.2	550	7	US-11-056-355B-105675	Sequence 105675, A	Sequence 105675, Application US-10-505-928-42
20	302	12.2	550	7	US-11-056-355B-116914	Sequence 116914, A	Sequence 116914, Application US-10-505-928-42
21	300.5	12.2	436	7	US-11-056-355B-34601	Sequence 34601, A	Sequence 34601, Application US-10-505-928-42
22	300.5	12.2	449	7	US-11-056-355B-24600	Sequence 54600, A	Sequence 54600, Application US-10-505-928-42
23	300.5	12.2	458	7	US-11-056-355B-51593	Sequence 54593, A	Sequence 54593, Application US-10-505-928-42
24	292	11.8	471	7	US-11-056-355B-79663	Sequence 79663, A	Sequence 79663, Application US-10-505-928-42
25	292	11.8	526	7	US-11-056-355B-79662	Sequence 79662, A	Sequence 79662, Application US-10-505-928-42

RESULT 2

Qy 355 AEIIIPFFVSRAPHECVELVDLFVRTVLVCLTCILAILIPRLDVLISVGVSSSALALI 414  
 ; TITLE OF INVENTION: ENCODED THERBY  
 ; FILE REFERENCE: 2750-1579PUS2  
 ; CURRENT APPLICATION NUMBER: US/10/953, 349  
 ; CURRENT FILING DATE: 2004-09-30  
 ; NUMBER OF SEQ ID NOS: 40252  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 368  
 ; LENGTH: 436  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-953-349-368

Query Match 18.9%; Score 465.5; DB 6; Length 436;  
 Best Local Similarity 32.4%; Pred: No. 8.2e-31;  
 Matches 143; Indels 77; Gaps 14;

Qy 371 AEIIIPGITSKFKHFKWQCFGIRSLFVLSITCGAILIPRLDVLISVGVSSSALALI 430  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HELIX RESEARCH INSTITUTE  
 ; TITLE OF INVENTION: Novel full length cDNA  
 ; FILE REFERENCE: H1-A106  
 ; CURRENT APPLICATION NUMBER: US/11/293, 697  
 ; CURRENT FILING DATE: 2005-12-05  
 ; PRIOR APPLICATION NUMBER: US/10/108, 260  
 ; PRIOR FILING DATE: 2002-03-28  
 ; NUMBER OF SEQ ID NOS: 5458  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 3609  
 ; LENGTH: 369  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-11-293-697-3609

Query Match 39.4%; Score 972.5; DB 7; Length 369;  
 Best Local Similarity 53.0%; Pred: No. 9e-73; Indels 27; Gaps 5;  
 Matches 196; Conservative 63; Mismatches 84; Indels 27; Gaps 5;

Qy 124 LESSPCSWLRLNHAHNGRRYDPEFLIVTOGRCVVYFVFLADNFKQV-----TEA 173  
 ; MEVPSWCLQKQAWGRSVDLIVTOGFCSCSYIYVFLAENYKQVHGFLESKVFTNS 60  
 ; NGTINNCHNNEBTVLPTMDRLSFLPFLVLVFLNRLAISFLSALITMVLISV 233  
 ; 61 TNSSNPCCR-----SVDRIMLCLFLPFLVFLVFLRELKNFLVSLANSMAYSV 113  
 ; 234 MIYOFIVORIPDPDSHLPLVAPWKTYPLFCTAISFEGIGMVLPLENKDKPRKFPLIY 293  
 ; Db 114 IYQYVVRNMPDPHNLPIVAGWKYPLFRTAVAFEGGVPLPLENQNEKSRFPQALN 173

Qy 294 LGMVIVTLYLISLGCLGYLOFGANIQGSTLNLPCNCWLYQSVKLISGIFTYALQFY 352  
 ; 174 IGMGVVTLVYVTLATIGYNCFRDEIKGSSLTNLQDWWYQSVKLISGIFTYSSQFY 233  
 ; 353 VPAELIIPFFVSRAPHECVELVDLFVRTVLVCLTCILAILIPRLDVLISVGVSSSALALI 412  
 ; 234 VPAELIIPGITSKFKHFKWQICEFIRSLFVLSITCGAILIPRLDVLISVGVSSSALALI 293

Qy 413 LIIPPLLEYTFYSEGMSPLTIFKDALISLGFYGVVFTYEALYELIOPS-----N 464  
 ; 294 LILPPLAELTFSKHYNINWVLKNISIAFTGVGFLGIGYITVBEIYPTPKVVAQTPO 353

Qy 465 APIF-INSTC 473  
 ; Db 354 SPFLNLNSTC 363

RESULT 3

US-10-953-349-368  
 ; Sequence 368, Application US/10953349  
 ; Publication No. US20060107345A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ALEXANDROV, Nickolai et al.  
 ; TITLE OF INVENTION: ENCODED THERBY  
 ; FILE REFERENCE: 2750-1579PUS2  
 ; CURRENT APPLICATION NUMBER: US/10/953, 349  
 ; CURRENT FILING DATE: 2004-09-30  
 ; NUMBER OF SEQ ID NOS: 40252  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 369  
 ; LENGTH: 371  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-953-349-369

Query Match 16.6%; Score 410.5; DB 6; Length 371;  
 Best Local Similarity 32.0%; Pred: No. 2.e-26;  
 Matches 132; Conservative 60; Mismatches 143; Indels 77; Gaps 14;

Qy 79 MGPISSLIGIVAVHCMGLIVKCAHHFCRRLNKS-----VYDGDFTVNGLESPCSW 131  
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES





PRIOR FILING DATE: 2002-12-11  
 NUMBER OF SEQ ID NOS: 56791  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 53486  
 LENGTH: 422  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 US-10-449-902-53486

Query Match 16.3%; Score 402.5; DB 6; Length 422;  
 Best Local Similarity 26.7%; Pred. No. 1.3e-25;  
 Matches 124; Conservative 79; Mismatches 191; Indels 71; Gaps 12;

Qy 28 GLNNLSSPQGSYQRF-----GQSNSTTWQTLILKGNIGTGLGLPLAVRNA 75  
 Db 2 GLGNASSSSSSRLIDPAPLLPHGCGDGAKLSSQPTPANVFIATVAGVGLGLPTFST 61  
 Qy 76 GIVMPISLJLJIGIVAHCMGILVKAHHFCRRLNK--SFVDYGDIVMXYLESSPCSWLR 133  
 Db 62 GWAAGSILLSSVVAALTFTYCMMLVACRRLADEHPKIASFGDGAVERG--P--- 112  
 Qy 134 NHAHMGRRVYVDFEFFLTVTQLGCCCCYVFVFLADNFKQVTEAANGTINCHNETVILTPMD 193  
 Db 113 3---GRLAYDTMVLISLQASPCVGYLIFISTMAYHYPVAPSSN-----ALLSP--- 157  
 Qy 194 SRLYMLSFPLPVLVFLYFLRNLRLSIFSLSLANITMLVSLIMIYQPTIVQRIPDPSHLPLVA 253  
 Db 158 KALFIWMLPFLQGLNSIKTILTLAPLSTADAVDVLGAMCVLGL-----EDVS 205  
 Qy 254 PW---KTYPLF-----FGTAIFSFSEGIGMVLPLNEKMDPRKFPLIYLGIVMIVT 300  
 Db 206 VWLAKPPPVFAFGGLSAILYLGIVGSYVAFSIGMVLPLAEAAKKKFGTGLSMGPIA 265  
 Qy 301 ILYISUGCLGYLOFSGANICOSITIUNLPNCMLYOSVKKLISIGIFTYALQFYVPAEITIP 360  
 Db 266 VMYGLFGAMXYTAEGDATRDITTTNGTGMWLSAAVQVLGCLCNLFTMPMMHPYEVAKR 325  
 Qy 361 FFVSRAPBPHCELVVDLFLPVTFLVCLTCILAILIPRLDVLISLGVSSSALLIPLLE 420  
 Db 326 LL--HGKRYC----WWLRLFLVLAVGSLAMVNPFTDFALVGSSVCVLFGLPVLPASPH 378  
 Qy 421 VTFVSESEGMSPLTIFKDALISLIGPFGVFGTYEALYELIQLPSNA 465  
 Db 379 LKVFGAE-MSWGVLSDDVLLVGLSLAVFGTYSLSLQIFHSSSA 422

RESULT 10  
 US-10-449-902-29254  
 Sequence 29254, Application US/10449902  
 Publication No. US20060123505A1  
 GENERAL INFORMATION:  
 APPLICANT: National Institute of Agrobiological Sciences.  
 APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 APPLICANT: The Institute of Physical and Chemical Research.  
 TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
 FILE REFERENCE: MOA-A02051-US  
 CURRENT APPLICATION NUMBER: US/10/449,902  
 CURRENT FILING DATE: 2003-05-29  
 PRIOR APPLICATION NUMBER: JP 2002-203269  
 PRIOR FILING DATE: 2002-05-30  
 PRIOR APPLICATION NUMBER: JP 2002-383870  
 PRIOR FILING DATE: 2002-12-11  
 NUMBER OF SEQ ID NOS: 56791  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 2954  
 LENGTH: 395  
 TYPE: PRT  
 ORGANISM: Oryza sativa  
 US-10-449-902-29254

Query Match 116; Conservative 75; Mismatches 158; Indels 72; Gaps 11;  
 Qy 51 OTLHLLKGNIIGTGLLGLPLAVKNAQIVNGPISLJIGIVAVHCMGILYVCAHHFCCRRL- 109  
 Db 39 KTFANVPIAVVGSGLGLPTFSRGTWAGSVLIAVAALTFLHCMILVACR---RRLA 94  
 Qy 110 --NKSFVDYGDIVMXYLESSPCSWLRNHAHMGRRVYDFEFFLTVTQLGFCCCYVFVFLADNFK 167  
 Db 95 YDHPIKIASFGD---LGAACV---GPAGRHTVDAMLVLQSASFVGYLIFISNTMA 143  
 Qy 168 QVIEANGTINCHNETVILTPMDR-LYMLSLPLFLVLFVFLRNLALSIFSSLANI 226  
 Db 144 HLYPVGDSSPS-----SPLITAKAIFIWNLPLFQIGLANSKTLTLAPLISFAGP 193  
 Qy 227 TMLVLVLMIVQFIVORIPDSHLPVLPAPWKYPLPFGTAFLSSEGIGMVLPLENKMDPR 286  
 Db 194 TEIL-----YGL--GVAYYAEGSIGMVLPLEAABDKR 224  
 Qy 287 KFPLILYLGIVTILYISLGCLGLYQFGANTIOGSITLNPNCWLYQSVLLYSIGIIFT 346  
 Db 225 KFGGTIALSNAFIAMNYGLEGAMGIAFLAFAATRDITTINGTGWMSVTVOGLCNLFFT 284  
 Qy 347 YALQF---YVPAEILIPFFYVSRAPEHCELVVFLYVCLTCILAILIPRLDVLIVS 403  
 Db 285 MPVMMNPVVAEIRL-----CRKEYAWNWRLLWNVGMAMLYVNPAFDPLSLV 334  
 Qy 404 GSVSSSALLIPLPLEVTTYSEGMSPLTIFKDALISLGFVGTGVGTYEALYELIOP 463  
 Db 335 GSSVCVLLGFLVLPAPAFHLKVFGAEVGPW-GLAGDVAVIVYGTALLAVSGTWTSLAQIFSSS 393  
 Qy 464 N 464  
 Db 394 D 394

RESULT 11  
 US-10-953-349-370  
 Sequence 370, Application US/109533349  
 Publication No. US2006010745A1  
 GENERAL INFORMATION:  
 APPLICANT: ALEXANDROV, Nikolai et al.  
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
 TITLE OF INVENTION: ENCODED THERBY  
 FILE REFERENCE: 2750-1579US2  
 CURRENT APPLICATION NUMBER: US/10/953,349  
 CURRENT FILING DATE: 2004-09-30  
 NUMBER OF SEQ ID NOS: 40252  
 SOFTWARE: PatentIn version 3.3  
 SEQ ID NO 370  
 LENGTH: 355  
 TYPE: PRT  
 ORGANISM: Arabidopsis thaliana  
 US-10-953-349-370

Query Match 15.5%; Score 382; DB 6; Length 355;  
 Best Local Similarity 32.8%; Pred. No. 5.1e-24;  
 Matches 122; Conservative 51; Mismatches 131; Indels 68; Gaps 12;

Qy 112 SFVDYGDIVMXYLESSPCSWLRNHAHMGRRVYDFEFFLTVTQLGFCCCYVFVFLADNFKQVIE 171  
 Db 23 SFGDGLFAV-----CGSL-----GRIVDLFITLSSAGFCGYLIFT----- 59  
 Qy 172 AANGT-NNCHNETVILTP-----MDSRLYMSFLPFLVLFVLFIRNL 214  
 Db 60 --GTTLANLSDPE---SPTSLRQFTRLGSEFGLGSSKSLYTGCFPFQGLUNSIKTL 112  
 Qy 215 RALSFSSLANI---TMLVLSYMIYQFTIVQRIPPSHLPVAPMRTPLF---FCTA 267  
 Db 113 THLAPLISIADIVDAGAVVIVEDSMILKQRPD----VVAAGGMSLFLYGNGVAVY 166  
 Qy 268 SPEGIGMVLPLENKMDPRKFPLIYLGLMVIVTILYISLGCLGYLOFGANTIQGSTLNLNP 327  
 Db 167 SPEGIGMVLPLESENKDKDGFKGKVIALGMFISLIIYAFGLGYLAFGEDIMDITANLG 226

Qy	328	NCWLYQSVKLSSYIGIFTYALQYVPAELIIPFVSRAPHECELVLDLFVRTVLVCLTC	387
Db	227	AGLISVTQVLQGLCMLNLFPLMMNPVFEIVERRP-SRG-----MYSAWLRWVLVLAVT	279
Qy	388	ILALIIPRLDVLISLGVSSAALALIIPPLIYVTFYSEGMSPLTFKDALISLISLGFVG	447
Db	280	LVAFLVPNFAFLSISLGVSSTCCVQFLALPHLVLVF-KEENGWLQMSSTDIAVVLGVVL	338
Qy	448	FVVGTYEALYEL 45.9	
Db	339	AVSGTWSLSEI 350	
RESULT 12			
US-10-449-902-32686			
Sequence 32286, Application US/10449902			
; GENERAL INFORMATION:			
; APPLICANT: National Institute of Agrobiological Sciences.			
; ADDRESS: 1-1, Higashimurayama, Tachikawa, Tokyo, 190-0005, Japan			
; FILING DATE: 2002-05-30			
; PRIORITY DATE: 2002-05-30			
; NUMBER OF SEQ ID NOS: 56791			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO: 32686			
; LENGTH: 342			
; TYPE: PRT			
; ORGANISM: Oryza sativa			
US-10-449-902-32686			
Query Match Score 339.5; DB 6; Length 342;			
Best Local Similarity 27.5%; Preid. No. 1. 6e-20; N matches 150; Indels 65; Gaps 12			
Matches 107; Conservative 67; N matches 150; Indels 65; Gaps 12			
Qy	95	MGILYVKCAHFCCRRLNK--SFVDYGDYTMYGLSSSPCSWLRNHAHWGRVYDFFLIVTQL	152
Db	1	MMLYVACRRLADEPKTKASGFDLGAFRG-----P-----GRLAVDTMVLISQA	46
Qy	153	GFCVCYFLVFLADNFQVIEANGTINCHNNETVLTPTMDSRVYMSFLPFLVILV	212
Db	47	SFCVGYLFLISNTMAHLYPVFAPSSN-----PLISP--KALFIWAMIPOLGINSIK	96
Qy	213	NLRALSIFSLLANTTMLVLISLVMYQFIVQRIQPDPSHLPLVAPW--KTYPLF-----	261
Db	97	TLLTIAPLSFADYDVLGAMWVLG-----EDVSWLAKPPVFAFGLSAIL	144
Qy	262	--FGTAIFSFEGIVNVLPLENKMIDPRKPLIYLGIVVITLNLISLGLCYLQFGANIQ	319
Db	145	YGIGVSYVAFGIVNVLPLAEAANKKKGTTLGLSMGFTIANYVGLFGAMGTYFGDTR	204
Qy	320	GSITUNLPCNWLQYKLYSIGFTYALQF--YVPABITPFFVSRAPHECELVVLD	376
Db	205	DITTNLGTGMLSAAVQGLCINLFTMPAAMHPPVYEAERLL----HGKRYC----W	254
Qy	377	FVRTVIVCLTCILAILIPRLDVLISLGVSSAALALIIPPLLETFYSEGMSPLTFK	436
Db	255	WLRWLVIVLAVGLSANYVNPNTDFALVGSSVCVNLGFVLPASFLKVGAE-MWSGVLS	313
Qy	437	DALISLGFVGFVQVGTYEALYELIOPSNA	465
Db	314	DVLTWLGKSLAFLVGTGTTTSLQTHSSAA	342

US-10-449-902-36917  
 Sequence 36917, Application US/104499802  
 Publication No. US2006012355A1  
 GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences, Sciences, Research, and Development, Institution.  
 ; APPLICANT: Bio-oriented Technology Research Advancement, Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205Y-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 36917  
 ; LENGTH: 349  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; US-10-449-902-36917

Query Match 13.4%; Score 332; DB 6; Length 349;  
 Best Local Similarity 27.6%; Pred. No. 6.8e-10;  
 Matches 96; Conservative 61; Mismatches 145; Indels 46; Gaps 9;

Qy	135 HAHW-----GRRVYDFFLIVTOLGFCFCYFVFLADNFQVIAANGTTNNCH 181
Db	21 HGHYTGYDGLGEKCFGTIGRCLETFILIVSQAGGSVYLIFQNL-----H 66
Qy	182 NBNBTVLPTMSRLNMSLFLVFLVLFIRNLRAISISSLANTMVLSVLVMYOFIVQ 241
Db	67 SVFSQMLSP--AAFPAILLPMQIALSFIRSLSSSPSFADCVNLLAMAIKEDLQ 123
Qy	.242 RIFDP--SHLPLVAPKTYPLUFFGTAIIFSFRGIGWYPLLENKMDRKFLPLIYLGIVIV 299
Db	124 LFDHPFANRSAFNGLW-AIPPTFGVAVFCFGFSMNLAESSMAERKFRWVLSQLAVVGI 182
Qy	300 TLYISIGCLGYLQFGANIQSITILNPNCLYQSYKLISIGIIFTYALQFYVPPAEIII 359
Db	183 IIVYACFGVCGTYLAYERGEATDITILNLPNSMSSAAVTKVGLCIALVTFPVNMHPTBIE 242
Qy	360 PFF-----VSRAPEHCELVVDLFLVRLCLTICLAILPLRLDVLISLVGSVSSSALL 411
Db	243 ERFQSSGGCFPKLUSHKVRGAEWVGLHSRRIVNTILSVASFTPAPRSFISVGSTCALL 302
Qy	412 ALIIPPLLEVTFYSGMSPLTIFKD--ALISLGFVGFVYGTBEALY 457
Db	303 SPTVLPITFHL-SIVGGSMSSPWRRGYGFLLFGPAGY--GLIRALF 347

RESULT 14  
 US-11-174-307B-5170  
 ; Sequence 5170, Application US/11174307B  
 ; Publication No. US20060143729A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BROVER, Vyacheslav  
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY  
 ; FILE REFERENCE: 2750-1601PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/174,307B  
 ; CURRENT FILING DATE: 2005-06-30  
 ; PRIOR APPLICATION NUMBER: 60/583,671  
 ; PRIOR FILING DATE: 2004-06-30  
 ; PRIOR APPLICATION NUMBER: 60/583,781  
 ; PRIOR FILING DATE: 2004-06-30  
 ; PRIOR APPLICATION NUMBER: 60/583,651  
 ; PRIOR FILING DATE: 2004-06-30  
 ; NUMBER OF SEQ ID NOS: 5544  
 ; SEQ ID NO: 5170

LENGTH: 531  
 TYPE: PRT  
 ORGANISM: *Triticum aestivum*  
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 LOCATION:  
 OTHER INFORMATION: PFam Name: Aa\_trans; PFam Description: Transmembrane amino acid transporter  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION:  
 OTHER INFORMATION: GI Number: 50904567; NR Description: putative amino acid transporter-like [Oryza sativa (japonica cultivar-group)]  
 OTHER INFORMATION: transport protein [Oryza sativa (japonica cultivar-group)]  
 OTHER INFORMATION: >gi|41053220|dbj|BAD08181.1| putative amino acid transport protein  
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 NAME/KEY: misc\_feature  
 LOCATION:  
 OTHER INFORMATION: GI Number: 50915446; NR Description: amino acid transporter  
 OTHER INFORMATION: transporter-like [Oryza sativa (japonica cultivar-group)]  
 OTHER INFORMATION: >gi|47497045|dbj|BAD19097.1| amino acid transporter-like [Oryza sativa (japonica cultivar-group)] >gi|47497767|dbj|BAD19867.1| putative amino acid transport protein  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION:  
 OTHER INFORMATION: GI Number: 30687791; NR Description: amino acid transporter  
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 OTHER INFORMATION: GI Number: 42563875; NR Description: amino acid transporter  
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 LOCATION:  
 OTHER INFORMATION: GI Number: 42563873; NR Description: amino acid transporter  
 US-11-17-307B-5170  
 Query Match 12.9%; Score 318; DB 7; Length 531;  
 Best Local Similarity 25.8%; Pred. No. 1.6e-18;  
 Matches 115; Conservative 73; Mismatches 175; Indels 82; Gaps 18;  
 Db 140 GQGSNTTWFOTLHLKGNTGTGLGLPLAVKNAGITGMGPISLLLIGIVAHRC--MGLLV 99  
 Db 100 KCAHHFCRRLNKSFDYGGDTMYGLESSPCSWLNRHAWGR--RVDDEFLIVTOLGFCCV 157  
 Db 194 K---HCFESKDGIATYD1-----GEAAFRGIGRLIISLILYTYEYSCV 235  
 Qy 42 GQSNSTTWFOTLHLKGNTGTGLGLPLAVKNAGITGMGPISLLLIGIVAHRC--MGLLV 99  
 Db 140 GQGSNTTWFOTLHLKGNTGTGLGLPLAVKNAGITGMGPISLLLIGIVAHRC--MGLLV 99  
 Db 100 KCAHHFCRRLNKSFDYGGDTMYGLESSPCSWLNRHAWGR--RVDDEFLIVTOLGFCCV 157  
 Db 215 RALSIFS--LLANITMVLSQLMI-----YQFIVORIPDPSHLPLVAPWKTYPLFFG 263  
 Db 285 RVLSYLSAGGGVATLWVFSVALGVGTGFGHQ-----TGEAVKWSGMPPFAIG 333  
 Qy 264 TAIFSEPGIGMVLPLEMKMDPRKEPLILYLGIVVITLILYISLGCLGYLOFGANTQGSTT 323  
 Db 334 IYGFCSGHSYSPNQYQSMSMRTKPKALFCFAVCTAIGSFAIGLNGFDKTLQSQT 393  
 Db 376 LFVRTVLVCLTCILAILIPRLDVLVISLGVSSSAALIIPPLLEVTTFYSEGMSPLTIF 435  
 Qy 324 LNLPNCWLYQSVKLLYS-IGIFFTVALQFTVPAELIIPFFVSRAPHC-----ELVVD 375  
 Db 394 LNLPKESFASTVALWTTVINPFTKFL-----LNP--LARSLEELRPEGFLNETIVS 444  
 Qy 376 LFVRTVLVCLTCILAILIPRLDVLVISLGVSSSAALIIPPLLEVTTFYSEGMSPLTIF 435  
 Db 445 IILRTSIVLAVSTVIAFLPFFGLWALIGLSLISLIVAVIMPALCFLKIAQNKATRQVIA 504  
 Qy 436 KDALISLGFVGFVNVGTYEALYELI 460  
 Db 505 SVAII-VGVISAALGTVSSPASII 528

Search completed: August 24, 2006, 01:30:25  
 Job time : 34 secs

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